GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 15, 2003, 06:15:44 ; Search time 367 Seconds
(without alignments)
9204.353 Million cell updates/sec

Title: US-09-043-944-5
Perfect score: 1500
Sequence: 1 gtttaattacccaagtttga.....taaaaaaaaaaaaaaaaaa 1500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1500	100.0	1500	18	AAT60306	Caenorhabditis ele
2	631	42.1	4137	24	AAL47322	C elegans sel-12 g
3	249.8	16.7	1750	18	AAT59536	Human early onset
4	249.8	16.7	1762	18	AAT59535	Human early onset
5	248.2	16.5	1392	19	AAX75761	Human presenilin I
6	248.2	16.5	1404	20	AAX90184	Human presenilin-1
7	248.2	16.5	1404	22	AAD10303	Human presenilin (
8	248.2	16.5	1488	18	AAT87402	Partial AD3 sequen
9	248.2	16.5	1703	19	AAV17357	PS1/429 protein co
10	248.2	16.5	2764	19	AAV29525	Homo sapiens PS-1
11	248.2	16.5	2764	19	AAV17358	PS1/467 protein co
12	248.2	16.5	2764	24	AAL47323	Presenilin coding
13	248.2	16.5	2765	17	AAT40028	Presenilin-1-1 wil
14	248.2	16.5	2765	18	AAT85332	Human S182 gene, P
15	248.2	16.5	2765	19	AAV04666	Human presenilin-1
16	248.2	16.5	2765	22	AAD18120	Human presenilin-1
17	248.2	16.5	2765	22	AAH74993	Nucleotide sequenc
18	247	16.5	1404	24	AAD27443	Human mutant prese
19	246.6	16.4	1911	18	AAT63207	Human S182 gene as
20	246.6	16.4	1914	18	AAT75576	Presenilin-1 VRSQ
21	246.6	16.4	3056	24	ABK83912	Human cDNA differe
22	246.6	16.4	3086	17	AAT40029	Presenilin-1-2, al
23	246.6	16.4	3086	19	AAV04667	Human presenilin-1
24	245	16.3	1750	19	AAV03246	Human presenilin I
25	245	16.3	2765	18	AAT85333	Human mutant S182
26	243.2	16.2	1404	20	AAX90185	Mouse presenilin-1
27	243.2	16.2	1964	17	AAT40030	Murine presenilin-
28	243.2	16.2	1964	19	AAV04668	Mouse presenilin-1
29	243.2	16.2	2681	18	AAT64819	Tumour suppressor
30	226.2	15.1	1895	17	AAT40043	Presenilin homolog
31	226.2	15.1	2048	23	ABL29237	Drosophila melanog
32	225.8	15.1	1404	24	AAD27444	Human mutant prese
33	225.8	15.1	2236	18	AAT51253	Human AD4 protein
34	225.8	15.1	2276	18	AAT87426	Full AD4/AD3LP seq
35	224.6	15.0	1404	24	AAD27445	Human mutant prese
36	224.2	14.9	1346	22	AAD10304	Human presenilin (
37	224.2	14.9	1347	24	AAD27447	Human mutant prese
38	224.2	14.9	1983	21	AAZ40670	Human presenilin-2
39	224.2	14.9	2144	21	AAZ40668	Human presenilin-2
40	224.2	14.9	2229	17	AAT40031	Human presenilin-2
41	224.2	14.9	2229	19	AAV04669	Human presenilin-2
42	224.2	14.9	2236	19	AAX75762	Human presenilin I
43	224.2	14.9	2236	22	AAD18121	Human presenilin-2
44	224.2	14.9	2236	22	AAH74994	Nucleotide sequenc
45	224.2	14.9	2527	22	AAH98480	Human EST-derived
46	221.4	14.8	1347	24	AAD27446	Human mutant prese
47	221.4	14.8	1347	24	AAD27448	Human mutant prese
48	192.8	12.9	1417	18	AAT87401	AD4/AD3LP sequence
49	192.2	12.8	1848	21	AAZ40671	Human presenilin-2
50	162.8	10.9	2002	21	AAZ40669	Human presenilin-2
51	119.2	7.9	510	21	AAZ40677	Human presenilin-2
52	108.8	7.3	1074	20	AAX25376	Caenorhabditis ele
53	97.6	6.5	945	17	AAT40037	Presenilin-1 exon
54	97.6	6.5	945	19	AAT99666	Human presenilin-1
55	95.4	6.4	2955	23	ABL29096	Drosophila melanog
56	95.4	6.4	4689	23	ABL29236	Drosophila melanog
57	87.6	5.8	819	21	AAZ46199	cDNA encoding a hu
58	83.2	5.5	2387	18	AAT51258	Human AD4 gene gen
59	82.8	5.5	48974	20	AAX55300	Mouse Presenilin-1
60	76.8	5.1	1487	21	AAC37775	Arabidopsis thalia
61	75.4	5.0	230	19	AAX11761	Human biallelic po
62	75.2	5.0	1058	21	AAC49040	Arabidopsis thalia
63	74.2	4.9	230	19	AAX12881	Human biallelic po
64	73.8	4.9	1362	21	AAC43427	Arabidopsis thalia
65	71.2	4.7	473	18	AAT51271	Human expressed se
66	69.8	4.7	121	22	ABA81374	PSEN1 mutation cor
C 67	69.8	4.7	121	22	ABA81375	PSEN1 mutation cor
68	69.8	4.7	121	22	ABA81378	PSEN1 mutation cor
C 69	69.8	4.7	121	22	ABA81379	PSEN1 mutation cor
70	68.8	4.6	121	22	ABA81366	PSEN1 mutation cor
C 71	68.8	4.6	121	22	ABA81367	PSEN1 mutation cor
72	67.8	4.5	121	22	ABA81370	PSEN1 mutation cor
C 73	67.8	4.5	121	22	ABA81371	PSEN1 mutation cor
74	61.4	4.1	2058	18	AAT51259	Human AD4 gene gen
C 75	60	4.0	626	23	ABV60941	Human prostate exp

ALIGNMENTS

RESULT 1
AAT60306

```
ID   AAT60306 standard; DNA; 1500 BP.
XX
AC   AAT60306;
XX
DT   11-JUL-1997  (first entry)
XX
DE   Caenorhabditis elegans SEL-12 gene.
XX
KW   SEL-12; presenilin; transgenic animal; Alzheimer's disease;
KW   animal model; therapy; diagnosis; ss.
XX
OS   Caenorhabditis elegans.
XX
FH   Key             Location/Qualifiers
FT   CDS             22..1407
FT                   /*tag=  a
XX
PN   WO9711956-A1.
XX
PD   03-APR-1997.
XX
PF   27-SEP-1996;    96WO-US15727.
XX
PR   27-SEP-1995;    95US-0004387.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Greenwald I,  Levitan D;
XX
DR   WPI; 1997-212841/19.
DR   P-PSDB; AAW14006.
XX
PT   New isolated SEL-12 presenilin gene - used to develop products for
PT   the diagnosis and prophylactic or therapeutic treatment of disorders
PT   such as Alzheimer's disease
XX
PS   Claim 11; Page 75-76; 99pp; English.
XX
CC   The sel-12 gene (AAT60306) of Caenorhabditis elegans (CE) encodes a
CC   polypeptide (AAW14006) that displays about 50% amino acid sequence
CC   identity to human presenilin PS1 and PS2 proteins associated with
CC   Alzheimer's disease (AD).  Like presenilins, sel-12 is widely
CC   expressed in neural and non-neural cells.  The gene was identified
CC   by screening for suppressors of the 'Multivulva' phenotype of CE
CC   caused by an allele of lin-12 that causes constitutive LIN-12
CC   activation.  2 Recessive suppressors, ar131 and ar133, proved to be
CC   alleles of the new gene (sel means suppressor and/or enhancer of
CC   lin-12).  The gene can be used to produce wild-type or mutated (see
CC   also AAW14007) SEL-12 in host cells, in methods for screening for
CC   extragenic suppressors or enhancers of a SEL-12 allele, and in the
CC   development of transgenic animals, esp. transgenic CE, useful in
CC   identifying cpds. that ameliorate AD.
XX
SQ   Sequence 1500 BP; 403 A; 312 C; 314 G; 471 T; 0 other;

  Query Match           100.0%;  Score 1500;  DB 18;  Length 1500;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1500;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTTTAATTACCCAAGTTTGAGATGCCTTCCACAAGGAGACAACAGGAGGGCGGAGGTGCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTTAATTACCCAAGTTTGAGATGCCTTCCACAAGGAGACAACAGGAGGGCGGAGGTGCA 60

Qy         61 GATGCGGAAACACATACCGTTTACGGTACAAATCTGATAACAAATCGGAATAGCCAAGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGCGGAAACACATACCGTTTACGGTACAAATCTGATAACAAATCGGAATAGCCAAGAA 120

Qy        121 GACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTA 180

Qy        181 TTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTT 240

Qy        241 TATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGT 300
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Db        241 TATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGT 300

Qy        301 ATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTT 360

Qy        361 CTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGA 420
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Db        361 CTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGA 420

Qy        421 TGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAA 480
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Qy        481 GTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAAC 540
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Qy        601 TACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGG 660
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Qy        661 ACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCA 720
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Db        661 ACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCA 720

Qy        721 AAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCG 780
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Db        721 AAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCG 780

Qy        781 GCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAAAC 840

Qy        841 ACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTGGA 900
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Db        841 ACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTGGA 900

Qy        901 GAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAAAA 960
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Qy        961 GTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGGAA 1020
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Qy       1021 CGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAGAG 1080
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Db       1021 CGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAGAG 1080

Qy       1081 GAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCGGC 1140
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Qy       1141 AAGGCTTCATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCATTCTTATC 1200
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Qy       1201 GGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGGCTCTGCAA 1260
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Qy       1261 TTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCACCCCATTTG 1320
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Db       1261 TTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCACCCCATTTG 1320
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Qy       1321 TTACACAAGTCTCTCAAAAGTGTTTATTATATTAATTCTCTGTTTTTGCCATTTCTTTGC 1380
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Qy       1381 ATCATCAACTTTTCGATTATATCTTGAGCGATCTCAAAGCTTTATTTTACATACCTATTT 1440
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Db       1381 ATCATCAACTTTTCGATTATATCTTGAGCGATCTCAAAGCTTTATTTTACATACCTATTT 1440

Qy       1441 ATTTTTGAACTTTGTCATTTAAGTTATATAAATAATTTATTAAAAAAAAAAAAAAAAAAA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ATTTTTGAACTTTGTCATTTAAGTTATATAAATAATTTATTAAAAAAAAAAAAAAAAAAA 1500
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RESULT 2
AAL47322
ID AAL47322 standard; DNA; 4137 BP.
XX
AC AAL47322;
XX
DT 02-SEP-2002 (first entry)
XX
DE C elegans sel-12 gene promoter and regulatory regions.
XX
KW Sel-12; presenilin; neuronal disorder; familial Alzheimer's disease;
KW amyloid precursor protein; APP; ds.
XX
OS Caenorhabditis elegans.
XX
PN US6376239-B1.
XX
PD 23-APR-2002.
XX
PF 04-APR-1997; 97US-0832867.
XX
PR 04-APR-1997; 97US-0832867.
XX
PA (ELEG-) ELEGENE GMBH.
XX
PI Baumeister R;
XX
DR WPI; 2002-478281/51.
XX
PT Isolated DNA molecule comprising promoter of the sel-12 gene from
PT Caenorhabditis elegans operably linked to heterologous gene, directs
PT expression in neural cells and is useful to develop drugs to treat
PT neuronal disorders -
XX
PS Claim 1; Fig 3; 78pp; English.
XX
CC The present invention relates to DNA molecules comprising the promoter of
CC the sel-12 gene from Caenorhabditis elegans operably linked to a
CC heterologous DNA sequence encoding a protein of interest. The sequence
CC can be used to develop drugs for the treatment, prevention or delay of a
CC neuronal disorder. In particular, the neuronal disorder may be familial
CC Alzheimer's disease. The present sequence is the C. elegans sel-12
CC promoter.
XX
SQ Sequence 4137 BP; 1252 A; 770 C; 703 G; 1412 T; 0 other;

Query Match 42.1%; Score 631; DB 24; Length 4137;
Best Local Similarity 83.3%; Pred. No. 6.7e-135;
Matches 822; Conservative 0; Mismatches 10; Indels 155; Gaps 3;

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Qy        267 ACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGAAGGGATTGATGTCACT 326
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Db       1579 ACTATACACTCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGAAGGGATTGATGTCACT 1638

Qy        327 TGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAGTTCTGCTGATTGTTTT 386
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Qy        387 CTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTGTCAGCAGTTTTCTTCT 446
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Db       1699 CTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTGTCAGCAGTTTTCTTCT 1758

Qy        447 TCTTTTCCTATTCACTACAATCTATGTGCA---------------------------- 476
              ||||||||||||||||||||||||||||||
Db       1759 TCTTTTCCTATTCACTACAATCTATGTGCAGTAAGTTGATATATTACTATTCTCATAAAA 1818

Qy        477 ---------------AGAAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGT 521
                            ||||||||||||||||||||||||||||||||||||||||||||||
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Qy        522 TTTGTTTGGACTGGGTAACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCC 581
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Qy        582 ATTGCGTCTGCAACAGTTCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTAT 641
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Qy        642 CAAGTACCTACCAGAATGGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCT 701
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1999 CAAGTACCTACCAGAATGGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCT 2058

Qy        702 GGTTGCCGTGCTCACACCAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAG 761
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2059 GGTTGCCGTGCTCACACCAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAG 2118

Qy        762 AAACGAGCCAATTTTCCCGGCGCTGATTTATTCGT------------------------- 796
              |||||||||||||||||||||||||||||||||
Db       2119 AAACGAGCCAATTTTCCCGGCGCTGATTTATTCGTGTAAGTTTCCTAATTTATGGAATTA 2178

Qy        797 ----------------------------------CTGGAGTCATCTATCCCTACGTTC 820
                                                 ||||||||||||||||||||||||
Db       2179 ATATTCATGACGTTTCAAATTCTAAAACATTTTCAGCTGGAGTCATCTATCCCTACGTTC 2238

Qy        821 TTGTTACTGCAGTTGAAAACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATA 880
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Db       2239 TTGTTACTGCAGTTGAAAACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATA 2298

Qy        881 ----------------------------------------------------CTTCTACAGCT 891
                                                                   ||||||||||||
Db       2299 GTGAGTATCACCTAAAATTTTCGAATTTTTATTCCAAAACTAATTTCAGCTTCTACAGCT 2358

Qy        892 TTTCCTGGAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATT 951
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Qy        952 CCTCAAAAAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTA 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2419 CCTCAAAAAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTA 2478

Qy       1012 AGGGTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGG 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2479 AGGGTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGG 2538

Qy       1072 CACGAAGAGGAAGAGAGAGGTGTGAAA 1098
              |||||||||||||||| |     |||
Db       2539 CACGAAGAGGAAGAGAGTGAGTGAAAA 2565
```

RESULT 3
AAT59536
ID AAT59536 standard; cDNA; 1750 BP.
XX
AC AAT59536;
XX
DT 07-MAY-1997 (first entry)
XX
DE Human early onset Alzheimer's disease (EOAD) splice variant gene.
XX
KW Early onset Alzheimer's disease; EOAD; neurodegenerative disease;
KW diagnosis; gene therapy; antisense; ds.
XX

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             174..1565
FT                   /*tag=  a
FT   variation       248..249
FT                   /*tag=  b
FT                   /label= VRSQ
FT                   /note= "splice site"
XX
PN   WO9703086-A1.
XX
PD   30-JAN-1997.
XX
PF   26-JUN-1996;    96WO-US11064.
XX
PR   18-JUL-1995;    95US-0001501.
PR   13-JUL-1995;    95US-0001142.
XX
PA   (UYSF-) UNIV SOUTH FLORIDA.
XX
PI   Hardy JA;
XX
DR   WPI; 1997-118980/11.
DR   P-PSDB; AAW11840.
XX
PT   Early onset Alzheimer's disease gene - useful for diagnosing a
PT   pre-disposition to Alzheimer's disease
XX
PS   Claim 1; Fig 2; 44pp; English.
XX
CC   A full-length cDNA (AAT59536) of the early onset Alzheimer's disease
CC   (EOAD) splice variant gene sequence codes for a 463-amino acid
CC   polypeptide (AAW11839).  Another full-length cDNA (AAT59535) of the
CC   EOAD gene codes for a 467-amino acid polypeptide (AAW11840).  The 2
CC   sequences can be used to generate primers and probes for the
CC   diagnosis of predisposition to Alzheimer's disease, esp. EOAD.
CC   They can also be used for prodn. of EOAD polypeptides in
CC   transformed host cells, and antisense sequences can be used for
CC   the treatment of EOAD.
XX
SQ   Sequence 1750 BP; 442 A; 389 C; 430 G; 478 T; 11 other;

  Query Match             16.7%;  Score 249.8;  DB 18;  Length 1750;
  Best Local Similarity   54.7%;  Pred. No. 1.4e-47;
  Matches  667;  Conservative    0;  Mismatches  512;  Indels   40;  Gaps    7;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||   |    ||||||| || ||    || || ||    |
Db        355 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 414

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | ||||| || ||| | || |||||||   |||| ||   ||| || ||  |  | | |
Db        415 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 474

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
              ||||||  |  ||  |||  |||| || | |    || ||       || || || |
Db        475 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 531

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
              | | |   |||  |   ||   ||| ||   ||||||  | ||||| |  | ||  | |
Db        532 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 591

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
              || | |||||  | || ||| | ||| ||||||||||||| ||  |||||| | || ||||
Db        592 TTGTCATGACTATCCTCCTGGTGGTTCTCTATAAATACAGGTGCTATAAGGTCATCCATG 651

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
              |||||||||  |      | |  |  | || ||| | ||  |    || ||  ||   |
Db        652 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 711

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
              ||||  | ||||  |   | ||  ||      |    |    |||    |     | | |

Db        712 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 771

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
              | | ||| ||  | |||||||| |  || ||||||||||||||| | || || || |||
Db        772 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 831

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
                || || |||| ||   ||| || ||||| ||||| ||||||||||||||| || ||||
Db        832 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 891

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
              |||||| |||| |  |  ||  ||| || || || |  ||| | || || ||  |    |
Db        892 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 951

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
              | ||||| ||| |  |      |||| ||||| || ||||||||||| ||  |  |||| |
Db        952 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1011

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
              | || || ||||| || ||   | |             | | | |||  || | ||  |
Db       1012 CAGCTCTCATTTACTCCTCAACAAT-------------GGTGTGGTTGGTGAATATGGCA 1058

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
                | || |     ||  ||| |       | ||  || || | | ||| |     | | | |
Db       1059 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1113

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
              |   |  . |    ||  | | | ||     ||  | | |||          |  |
Db       1114 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1171

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
                | |     |  | |     ||||       |   |  | | ||  |     |
Db       1172 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1231

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
              |   |  |||  |     |    ||| | |||             |     | | ||
Db       1232 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1281

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
                || || || || || |||||||  |||| || ||||||||||||  ||||||  | |
Db       1282 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1341

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
              | || || |      || |          |||||||||||| || || || |||| || ||||
Db       1342 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1401

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
              |  | || ||| | ||| | ||  |  | || || ||| | |||||  |||| | || |
Db       1402 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1461

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
              ||||  |||| |||||   ||  || ||  |||| ||||||   ||    |  | |
Db       1462 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1521

Qy       1312 CCCCATTTGTTACACAAGT 1330
                || ||| |    ||| |
Db       1522 AGCCTTTTATGGACCAATT 1540


RESULT 4
AAT59535
ID   AAT59535 standard; cDNA; 1762 BP.
XX
AC   AAT59535;
XX
DT   07-MAY-1997  (first entry)
XX
DE   Human early onset Alzheimer's disease (EOAD) gene.
XX
KW   Early onset Alzheimer's disease; EOAD; neurodegenerative disease;
KW   diagnosis; gene therapy; antisense; ds.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
FT   CDS             174..1577
FT                   /*tag= a
FT   variation       249..260
FT                   /*tag= b
FT                   /label= VRSQ
FT                   /note= "splice variant"
XX
PN   WO9703086-A1.
XX
PD   30-JAN-1997.
XX
PF   26-JUN-1996;   96WO-US11064.
XX
PR   18-JUL-1995;   95US-0001501.
PR   13-JUL-1995;   95US-0001142.
XX
PA   (UYSF-) UNIV SOUTH FLORIDA.
XX
PI   Hardy JA;
XX
DR   WPI; 1997-118980/11.
DR   P-PSDB; AAW11839.
XX
PT   Early onset Alzheimer's disease gene - useful for diagnosing a
PT   pre-disposition to Alzheimer's disease
XX
PS   Claim 1; Fig 1; 44pp; English.
XX
CC   A full-length cDNA (AAT59535) of the early onset Alzheimer's disease
CC   (EOAD) gene sequence codes for a 467-amino acid polypeptide (AAW11839).
CC   Another full-length cDNA (AAT59536) of an EOAD splice variant gene
CC   codes for a 463-amino acid polypeptide (AAW11840).  The 2 sequences
CC   can be used to generate primers and probes for the diagnosis of
CC   predisposition to Alzheimer's disease, esp. EOAD.  They can also be
CC   used for prodn. of EOAD polypeptides in transformed host cells, and
CC   antisense sequences can be used for the treatment of EOAD.
XX
SQ   Sequence 1762 BP; 442 A; 389 C; 430 G; 478 T; 23 other;
```

Query Match 16.7%; Score 249.8; DB 18; Length 1762;
Best Local Similarity 54.7%; Pred. No. 1.4e-47;
Matches 667; Conservative 0; Mismatches 512; Indels 40; Gaps 7;

```
Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db        367 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 426

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db        427 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 486

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db        487 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 543

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db        544 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 603

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db        604 TTGTCATGACTATCCTCCTGGTGGTTCTCTATAAATACAGGTGCTATAAGGTCATCCATG 663

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db        664 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 723

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db        724 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 783

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db        784 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 843

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db        844 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 903

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db        904 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 963

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db        964 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1023

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db       1024 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1070

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db       1071 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1125

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db       1126 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1183

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db       1184 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1243

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db       1244 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1293

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db       1294 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1353

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db       1354 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1413

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db       1414 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1473

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db       1474 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1533

Qy       1312 CCCCATTTGTTACACAAGT 1330
Db       1534 AGCCTTTTATGGACCAATT 1552
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RESULT 5
AAX75761
ID   AAX75761 standard; DNA; 1392 BP.
XX
AC   AAX75761;
XX
DT   22-JUL-1999  (first entry)
XX
DE   Human presenilin I DNA.
XX
KW   Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW   frameshift mutation; age-related disease; neurodegenerative disorder;
KW   Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW   Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW   diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW   ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
```

KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A; ss.
XX
OS Homo sapiens.
XX
PN WO9845322-A2.
XX
PD 15-OCT-1998.
XX
PF 02-APR-1998; 98WO-IB00705.
XX
PR 10-APR-1997; 97US-0043163.
XX
PA (UYUT-) RIJKSUNIV UTRECHT.
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
XX
DR WPI; 1998-609901/51.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also
PT for treatment and prevention with specific ribozymes or wild-type
PT RNA
XX
PS Disclosure; Figure 10; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases,
CC especially cancer and a wide range of neurodegenerative disorders (e.g.
CC Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's
CC disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus
CC type II and many others listed) or susceptibility to these disorders. The
CC method allows a definitive diagnosis of Alzheimer's disease in living
CC patients, at an early stage. It is based on the observation that disease
CC may be caused by mutations in RNA rather than DNA. The invention
CC describes the used of neuronal system RNA molecules, specifically
CC proteins including beta-amyloid precursor protein (beta-APP), the
CC microtubule associated proteins Tau and Big Tau, ubiquitin B,
CC apolipoprotein E, microtubule associated protein 2 (MAP2),
CC neurofilament-L, neurofilament-M, neurofilament-F, presenilin I,
CC presenilin II, glial fibrillary acidic protein (GFAP), the cellular
CC tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene,
CC semaphorin III, HUPF-1, high mobility group protein-C (HMGP-C) and
CC neuroendocrine specific protein A. This sequence encodes the wild type
CC and mutant protein fragments represented in AAY20854-Y20895.
XX
SQ Sequence 1392 BP; 359 A; 310 C; 333 G; 390 T; 0 other;

Query Match 16.5%; Score 248.2; DB 19; Length 1392;
Best Local Similarity 54.6%; Pred. No. 3.1e-47;
Matches 666; Conservative 0; Mismatches 513; Indels 40; Gaps 7;

```
Qy      119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db      182 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 241

Qy      179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db      242 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 301

Qy      239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db      302 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 358

Qy      299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db      359 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 418

Qy      359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db      419 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 478

Qy      419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db      479 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 538

Qy      479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db      539 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 598

Qy      539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db      599 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 658

Qy      599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db      659 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 718

Qy      659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db      719 GGAGTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 778

Qy      719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db      779 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCCCAGGAGAGAAATGAAACGCTTTTTC 838

Qy      779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db      839 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 885

Qy      839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db      886 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 940

Qy      899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db      941 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 998

Qy      959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db      999 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1058

Qy      1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db      1059 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1108

Qy      1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db      1109 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1168

Qy      1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db      1169 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1228

Qy      1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db      1229 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1288

Qy      1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db      1289 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1348

Qy      1312 CCCCATTTGTTACACAAGT 1330
Db      1349 AGCCTTTTATGGACCAATT 1367
```

RESULT 6
AAX90184
ID AAX90184 standard; DNA; 1404 BP.

```
XX
AC   AAX90184;
XX
DT   23-SEP-1999  (first entry)
XX
DE   Human presenilin-1 encoding DNA.
XX
KW   Presenilin-1; mutation; gene mutant animal; Alzheimer's disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9934670-A1.
XX
PD   15-JUL-1999.
XX
PF   07-JAN-1999;   99WO-JP00015.
XX
PR   08-JAN-1998;   98JP-0002191.
XX
PA   (DAUC ) DAIICHI PHARM CO LTD.
XX
PI   Takeda J,  Takeda M;
XX
DR   WPI; 1999-430307/36.
DR   P-PSDB; AAY24419.
XX
PT   Mutant presenilin-1 gene-introduced animals, useful as model animals
PT   for study of Alzheimer's diseases in human and screening substances
PT   for prevention and/or treatment of the diseases
XX
PS   Disclosure; Page 53-54; 64pp; Japanese.
XX
CC   The present invention describes a gene mutant animal having a non-human
CC   mutant presenilin gene. The mutant presenilin gene causes amino acid
CC   substitutions at 1 or more positions of 79, 82, 96, 115, 120, 135, 139,
CC   143, 146, 163, 209, 213, 231, 235, 246, 250, 260, 263, 264, 267, 269,
CC   280, 285, 286, 290, 318, 384, 392, 410, 426 and 436, with corresponding
CC   N-terminals being e.g. A79V, V82L, A426 and P436S, particularly by
CC   replacing isoleucine of position 213 by another amino-acid especially
CC   threonine. The gene mutant animals e.g. mice can be used as model
CC   animals for the study of human Alzheimer's diseases and to screen and
CC   evaluate substances as candidates for prevention and/or therapy of
CC   Alzheimer's diseases in patients. They can over-produce amyloid
CC   beta protein by the presenilin-1 gene to cause nerve cell death or
CC   peeling off in the hippocampus earlier. Such animals are being
CC   pathologically close to human patients with Alzheimer's diseases. The
CC   present sequence encodes human presenilin-1, as given in the present
CC   invention.
XX
SQ   Sequence 1404 BP; 362 A; 312 C; 337 G; 393 T; 0 other;

  Query Match             16.5%;  Score 248.2;  DB 20;  Length 1404;
  Best Local Similarity   54.6%;  Pred. No. 3.1e-47;
  Matches  666;  Conservative    0;  Mismatches  513;  Indels   40;  Gaps    7;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db        194 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 253

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db        254 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 313

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db        314 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 370

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db        371 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 430

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db        431 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 490

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db        491 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 550

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db        551 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 610

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db        611 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 670

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db        671 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 730

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db        731 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 790

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db        791 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 850

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db        851 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 897

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db        898 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 952

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db        953 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1010

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db        1011 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1070

Qy        1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db        1071 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1120

Qy        1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db        1121 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1180

Qy        1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db        1181 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1240

Qy        1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db        1241 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1300

Qy        1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db        1301 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1360

Qy        1312 CCCCATTTGTTACACAAGT 1330
Db        1361 AGCCTTTTATGGACCAATT 1379


RESULT 7
AAD10303
ID   AAD10303 standard; DNA; 1404 BP.
XX
AC   AAD10303;
XX
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```
DT   24-SEP-2001  (first entry)
XX
DE   Human presenilin (PS1) DNA.
XX
KW   Human; Par-4; presenilin; PS1; neuroprotective; nuclear factor kappa B;
KW   NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis;
KW   peripheral neuropathy; motorneuron disorder; neurodegenerative disorder;
KW   Parkinson's disease; Meniere's disease; multiple sclerosis; Bell's palsy;
KW   Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;
KW   nerve deafness; Alzheimer's disease; epilepsy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1404
FT                   /*tag= a
FT                   /product= "Human presenilin PS1 protein"
XX
PN   WO200151671-A2.
XX
PD   19-JUL-2001.
XX
PF   08-JAN-2001; 2001WO-US00526.
XX
PR   10-JAN-2000; 2000US-0175200.
PR   04-JAN-2001; 2001US-0754949.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Mccarthy J,  Cordell B;
XX
DR   WPI; 2001-451872/48.
DR   P-PSDB; AAE05466.
XX
PT   Identifying inhibitors of neuronal degeneration useful for treating
PT   e.g. Alzheimer's disease, by determining the ability of a compound to
PT   induce nuclear factor kappa B activation, with the involvement of
PT   presenilin or Par-4  -
XX
PS   Claim 3; Page 59-60; 66pp; English.
XX
CC   The invention relates to human Par-4 protein, presenilin protein (PS1
CC   and PS2) and their corresponding DNA molecules. The invention also
CC   relates to a method for identifying inhibitors of neuronal degeneration,
CC   comprising cotransfecting eukaryotic host cells expressing presenilin
CC   (PS), with a Par-4 DNA, and an NF-kappa B dependent reporter construct,
CC   exposing the cotransfected cells to a candidate molecule and monitoring
CC   the ability of the candidate molecule to induce NF-kappa B activation.
CC   Presenilin proteins participates in nuclear factor kappa B (NF-kappa B)
CC   signalling and activation. The inhibitors of neuronal degeneration
CC   are useful for treating neurodegenerative disorders such as Alzheimer's
CC   disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's
CC   chorea, Down's syndrome, nerve deafness, Meniere's disease and also for
CC   treating peripheral neuropathies, motorneuron disorders such as
CC   amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions
CC   involving spinal muscular atrophy and paralysis. The present DNA sequence
CC   encodes human presenilin (PS1) protein.
XX
SQ   Sequence 1404 BP; 362 A; 312 C; 337 G; 393 T; 0 other;

  Query Match           16.5%;  Score 248.2;  DB 22;  Length 1404;
  Best Local Similarity  54.6%;  Pred. No. 3.1e-47;
  Matches  666;  Conservative    0;  Mismatches  513;  Indels   40;  Gaps    7;

Qy       119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
            |||| ||  | |  |  || ||   |    ||||||| || ||    || || ||    |
Db       194 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 253

Qy       179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
            |.|||| || ||| | || |||||||   |||| ||   ||| || ||  |  | | |
Db       254 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 313

Qy       239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
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            ||||||  |  ||  |||   ||||  || | |     || ||       || || || |
Db*      314 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 370

Qy       299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
             | | |   |||  |   ||  ||| ||  ||||||  | |||||  |  | ||  | |
Db       371 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 430

Qy       359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
             || | |||||  | || ||| | ||| | |||||||||| ||  ||||||  | || ||||
Db       431 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 490

Qy       419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
               |||||||| |      | |  |  | || ||| | ||  |    || ||  ||  |
Db       491 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 550

Qy       479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
             ||||  | ||||  |  | || ||     |    |  |||    |    | | |
Db       551 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 610

Qy       539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
             | | ||| ||  | |||||||| |  || || |||||||||||| | || || || |||
Db       611 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 670

Qy       599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
             || || |||| ||  ||| || ||||| ||||| |||||||||||||| || ||||
Db       671 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 730

Qy       659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
             |||||| |||| |  |  ||  ||| || || || |  ||| | || || ||  |   |
Db       731 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 790

Qy       719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
             | ||||| ||| |  |     |||| ||||| || ||||||||||| ||  |  |||| |
Db       791 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 850

Qy       779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
             | || || ||||| || ||   | |              | | | |||  || |  ||  |
Db       851 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 897

Qy       839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
             | || |     ||  ||| |     |  ||  || || | ||| |    |  | | | |
Db       898 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 952

Qy       899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
             |   |     |    || | | | ||     ||  | | |||           | |
Db       953 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1010

Qy       959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
               | |     |  | |     ||||        |   |  | | || |      |
Db      1011 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1070

Qy      1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
             |   |  |||  |     |   ||| | |||                |     | | ||
Db      1071 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1120

Qy      1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
               || || || || || |||||||||  |||| ||  |||||||||||||  ||||||  | |
Db      1121 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1180

Qy      1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
             | || || |      || |       |||||||||| || || || ||||  || ||||
Db      1181 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1240

Qy      1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
             |  | || ||| | ||| | ||  |  | || || ||| | |||||   |||| | || |
Db      1241 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1300

Qy      1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
             |||| |||| |||||   ||  || ||  |||| ||||||   ||     |   | |
Db      1301 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1360

Qy      1312 CCCCATTTGTTACACAAGT 1330
               || ||| |    ||| |
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Db       1361 AGCCTTTTATGGACCAATT 1379

RESULT 8
AAT87402
ID   AAT87402 standard; DNA; 1488 BP.
XX
AC   AAT87402;
XX
DT   07-DEC-1997  (first entry)
XX
DE   Partial AD3 sequence.
XX
KW   AD3; AD4/AD3LP; Alzheimer's disease; chromosome; missegregation;
KW   presenilin; inhibitor; AD; trisomy 21; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1225
FT                   /*tag= a
FT                   /note= "C-terminal"
XX
PN   WO9707213-A2.
XX
PD   27-FEB-1997.
XX
PF   15-AUG-1996;   96WO-US13314.
XX
PR   16-AUG-1995;   95US-0002448.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Li J,  Potter H;
XX
DR   WPI; 1997-165297/15.
DR   P-PSDB; AAW28507.
XX
PT   Identifying genes which cause chromosome missegregation - useful for
PT   identifying causes of and treatments for diseases, e.g. Alzheimer's
PT   disease, cancer and ageing
XX
PS   Claim 21; Fig 1; 77pp; English.
XX
CC   Identifying genes which cause improper chromosome segregation,
CC   screening for inhibitors of chromosome missegregation and processes
CC   caused by genes encoding chromosome missegregation promoters
CC   was exemplified using Alzheimer's disease.  The sequences
CC   given in AAT87401 to AAT87426 can be used in the above methods.
XX
SQ   Sequence 1488 BP; 374 A; 321 C; 354 G; 439 T; 0 other;

  Query Match             16.5%;  Score 248.2;  DB 18;  Length 1488;
  Best Local Similarity   54.6%;  Pred. No. 3.2e-47;
  Matches  666;  Conservative    0;  Mismatches  513;  Indels   40;  Gaps    7;

Qy       119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db        15 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC  74

Qy       179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db        75 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 134

Qy       239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db       135 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 191

Qy       299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db       192 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 251

Qy       359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418

Db       252 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 311

Qy       419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db       312 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 371

Qy       479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db       372 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 431

Qy       539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db       432 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 491

Qy       599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db       492 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 551

Qy       659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db       552 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 611

Qy       719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db       612 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 671

Qy       779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db       672 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 718

Qy       839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db       719 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 773

Qy       899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db       774 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 831

Qy       959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db       832 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 891

Qy      1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db       892 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 941

Qy      1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db       942 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1001

Qy      1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db      1002 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1061

Qy      1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db      1062 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1121

Qy      1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db      1122 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1181

Qy      1312 CCCCATTTGTTACACAAGT 1330
Db      1182 AGCCTTTTATGGACCAATT 1200

RESULT 9
AAV17357
ID   AAV17357 standard; DNA; 1703 BP.
XX
AC   AAV17357;
```

```
XX
DT   04-JUN-1998  (first entry)
XX
DE   PS1/429 protein coding sequence.
XX
KW   Presenilin peptide; PS1/429; immunogen; immune response; PS1 gene;
KW   Alzheimer's disease; mitochondrial pathology; neurodegeneration;
KW   apoptosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             152..1441
FT                   /*tag= a
XX
PN   WO9746678-A1.
XX
PD   11-DEC-1997.
XX
PF   03-JUN-1997;    97WO-US09272.
XX
PR   18-JUL-1996;    96US-0683315.
PR   06-JUN-1996;    96US-0659296.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Chisholm JC,  Davis JN,  Drache B;
XX
DR   WPI; 1998-042186/04.
DR   P-PSDB; AAW41429.
XX
PT   DNA encoding presenilin peptide PS1/429 and its analogues - useful
PT   for diagnosis and treatment of Alzheimer's disease
XX
PS   Claim 5; Fig 1; 77pp; English.
XX
CC   This sequence encodes the PS1/429 presenilin peptide (II) of the
CC   invention. Cells transformed with the DNA are used to produce recombinant
CC   (II) and analogues, useful e.g. as immunogens for generating an immune
CC   response against PS1/429. (II) is a new product of the PS1 gene,
CC   mutations in which cause Alzheimer's disease (AD). The nucleic acids are
CC   generally useful as probes for detection and quantification of PS1/429,
CC   particularly for diagnosis of AD, especially the target sequences that
CC   hybridise with probes are isolated for sequencing. Antibodies (Ab) can
CC   also be diagnosed at the protein level using Ab as immunoassay reagents.
CC   Ab can also be used to identify epitopes and for affinity purification of
CC   peptides. Antisense nucleic acid may also be used to regulate expression
CC   of the PS1/429 gene, and both nucleic acids and peptides are useful as
CC   size markers in electrophoresis, chromatography etc. The transgenic
CC   animals are used as models for AD, e.g. for testing drugs. Regulators of
CC   the PS1/429 gene or polypeptide can be used to treat e.g. AD or diseases
CC   involving mitochondrial pathology, apoptosis and neurodegeneration.
CC   Typical regulators are antisense sequences, ribozymes, aptamers,
CC   synthetic or natural compounds. (II) may also be used to target other
CC   coding sequences to particular cellular locations.
XX
SQ   Sequence 1703 BP; 434 A; 372 C; 418 G; 479 T; 0 other;

  Query Match          16.5%;  Score 248.2;  DB 19;  Length 1703;
  Best Local Similarity   54.6%;  Pred. No. 3.3e-47;
  Matches  666;  Conservative    0;  Mismatches  513;  Indels   40;  Gaps    7;

Qy       119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db       231 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 290

Qy       179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db       291 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 350

Qy       239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db       351 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 407

Qy       299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db       408 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 467

Qy       359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db       468 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 527

Qy       419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db       528 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 587

Qy       479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db       588 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 647

Qy       539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db       648 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 707

Qy       599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db       708 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 767

Qy       659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db       768 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 827

Qy       719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db       828 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 887

Qy       779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db       888 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 934

Qy       839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db       935 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 989

Qy       899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db       990 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1047

Qy       959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db      1048 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1107

Qy      1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db      1108 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1157

Qy      1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db      1158 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1217

Qy      1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db      1218 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1277

Qy      1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db      1278 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1337

Qy      1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db      1338 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1397

Qy      1312 CCCCATTTGTTACACAAGT 1330
Db      1398 AGCCTTTTATGGACCAATT 1416
```

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RESULT 10
AAV29525
ID   AAV29525 standard; cDNA; 2764 BP.
XX
AC   AAV29525;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Homo sapiens PS-1 cDNA.
XX
KW   PS-1; presenilin; presenilin-1; PSP-1; Alzheimer's disease;
KW   serine protease; neurodegeneration; predisposition; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             249..1652
FT                   /*tag=  a
FT                   /product= PS-1
XX
PN   EP828003-A2.
XX
PD   11-MAR-1998.
XX
PF   26-AUG-1997;   97EP-0306501.
XX
PR   13-DEC-1996;   96US-0032875.
PR   06-SEP-1996;   96US-0025436.
PR   25-OCT-1996;   96US-0027873.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Browne MJ,  Clinkenbeard HE,  Creasy CL,  Karran EH;
PI   Livi GP,  Southan CD;
XX
DR   WPI; 1998-161101/15.
DR   P-PSDB; AAW56770.
XX
PT   Nucleic acids encoding human serum protease protein(s) - used for
PT   diagnosing pre-disposition to Alzheimer's disease, etc.
XX
PS   Example 1; Page 24-25; 65pp; English.
XX
CC   The sequence is that of encoding the presenilin PS-1 which was used
CC   in the cloning and isolation of the serine protease PSP1.
XX
SQ   Sequence 2764 BP; 715 A; 623 C; 652 G; 773 T; 1 other;

  Query Match           16.5%;  Score 248.2;  DB 19;  Length 2764;
  Best Local Similarity   54.6%;  Pred. No. 3.8e-47;
  Matches  666;  Conservative    0;  Mismatches  513;  Indels   40;  Gaps    7;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||   |    ||||||| || ||    || || ||    |
Db        442 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 501

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | |||||  || ||| | || |||||||   |||| ||   ||| || ||  |  | |  |
Db        502 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 561

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
              ||||||  |  ||  |||   |||| || | |     || ||       || || || | |
Db        562 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 618

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
                | | |   |||  |   ||  ||| ||  ||||||  | ||||| |  | ||  | |
Db        619 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 678

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
              || | |||||  | || ||| | ||| | ||||||||| ||  ||||||  | || ||||
Db        679 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 738

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
              |||||||| |       | |  |  | || ||| | ||  |    || ||  ||   |
Db        739 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 798

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
              ||||  | ||||  |   | ||  ||       |     |     |||     |    | | |
Db        799 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 858

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
              | | ||| ||  | |||||||| |  || || ||||||||||||| | || || || |||
Db        859 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 918

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
              || || ||||  ||   ||| || ||||| ||||| |||||||||||||| || ||||
Db        919 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 978

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
              ||||||  |||| |  |  ||  ||| || || || |  ||| | || || ||  |   |
Db        979 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1038

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
              | ||||| ||| |  |     |||| ||||| || ||||||||||| ||  |  |||| |
Db       1039 CGAAAGGTCCACTTGGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1098

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
              | || || ||||| || ||   | |             | | | |||  || |  ||  |
Db       1099 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 1145

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
              | || |    ||  ||| |     |  ||  || || | ||| |    |  | | |
Db       1146 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1200

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
              |    |     |   ||  | | | ||     ||  | | |||          |  |
Db       1201 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1258

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
              | |     | | |     ||||       |   |  | | || |     |
Db       1259 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1318

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
              |   | |||  |    |   ||| | |||                |     | | ||
Db       1319 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1368

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
              || || || || || ||||||||  |||| || ||||||||||||  ||||||  | |
Db       1369 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1428

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
              | || || |      || |       |||||||||| || || || ||||  || ||||
Db       1429 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1488

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
              |  | || ||| | ||| | ||  |  | || || ||| | |||||   |||| | || |
Db       1489 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1548

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
              ||||  |||| |||||   || || ||  |||| ||||||    ||    |  | |
Db       1549 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1608

Qy       1312 CCCCATTTGTTACACAAGT 1330
              || ||| |    ||| |
Db       1609 AGCCTTTTATGGACCAATT 1627


RESULT 11
AAV17358
ID   AAV17358 standard; DNA; 2764 BP.
XX
AC   AAV17358;
XX
DT   04-JUN-1998  (first entry)
```

XX
DE PS1/467 protein coding sequence.
XX
KW Presenilin peptide; PS1/429; immunogen; immune response; PS1 gene;
KW Alzheimer's disease; mitochondrial pathology; neurodegeneration;
KW apoptosis; PS1/467; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 249..1652
FT /*tag= a
XX
PN WO9746678-A1.
XX
PD 11-DEC-1997.
XX
PF 03-JUN-1997; 97WO-US09272.
XX
PR 18-JUL-1996; 96US-0683315.
PR 06-JUN-1996; 96US-0659296.
XX
PA (FARB) BAYER CORP.
XX
PI Chisholm JC, Davis JN, Drache B;
XX
DR WPI; 1998-042186/04.
DR P-PSDB; AAW41430.
XX
PT DNA encoding presenilin peptide PS1/429 and its analogues - useful
PT for diagnosis and treatment of Alzheimer's disease
XX
PS Disclosure; Fig 2; 77pp; English.
XX
CC This sequence encodes the PS1/467 presenilin peptide. This sequence is
CC specifically stated as not being in the nucleic acid of the invention,
CC which encodes the PS1/429 presenilin peptide PS1/429 (II). Cells
CC transformed with the DNA are used to produce recombinant (II) and
CC analogues, useful e.g. as immunogens for generating an immune response
CC against PS1/429. (II) is a new product of the PS1 gene, mutations in
CC which cause Alzheimer's disease (AD). The nucleic acids are generally
CC useful as probes for detection and quantification of PS1/429,
CC particularly for diagnosis of AD, especially the target sequences that
CC hybridise with probes are isolated for sequencing. Antibodies (Ab) can
CC also be diagnosed at the protein level using Ab as immunoassay reagents.
CC Ab can also be used to identify epitopes and for affinity purification of
CC peptides. Antisense nucleic acid may also be used to regulate expression
CC of the PS1/429 gene, and both nucleic acids and peptides are useful as
CC size markers in electrophoresis, chromatography etc. The transgenic
CC animals are used as models for AD, e.g. for testing drugs. Regulators of
CC the PS1/429 gene or polypeptide can be used to treat e.g. AD or diseases
CC involving mitochondrial pathology, apoptosis and neurodegeneration.
CC Typical regulators are antisense sequences, ribozymes, aptamers,
CC synthetic or natural compounds. (II) may also be used to target other
CC coding sequences to particular cellular locations.
XX
SQ Sequence 2764 BP; 715 A; 624 C; 653 G; 772 T; 0 other;

Query Match 16.5%; Score 248.2; DB 19; Length 2764;
Best Local Similarity 54.6%; Pred. No. 3.8e-47;
Matches 666; Conservative 0; Mismatches 513; Indels 40; Gaps 7;

```
Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||   |    ||||||| || ||    || || ||    |
Db        442 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 501

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | ||||| || ||| | || |||||||   |||| ||  ||| || ||  |  | |  |
Db        502 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 561

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
              ||||||  |  ||  |||   ||||  || | |     || ||       || || || |
Db        562 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 618

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
              | | |   |||  |   ||   ||| ||  ||||||  | |||||  |  | ||  | |
Db        619 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 678

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
              || | |||||  | || ||| | ||| | |||||||||| ||  |||||| | || ||||
Db        679 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 738

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
                |||||||||  |      | |  |  | || ||| | ||  |    || ||  ||  |
Db        739 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 798

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
              ||||  | ||||  |   | ||  ||      |    |    |||    |     |  | |
Db        799 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 858

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
              | | ||| ||  | |||||||| |  || || ||||||||||||  | || || || |||
Db        859 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 918

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
                || || |||  ||  ||| || ||||| |||| |||||||||||||| || ||||
Db        919 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 978

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
              |||||| |||| |  | ||  ||| || || || |  ||| | || || || |    |
Db        979 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1038

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
              | ||||| ||| |  |      |||| ||||| || |||||||||| ||  |  |||| |
Db        1039 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1098

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
              | || || ||||| || ||   | |              | | | |||  || | |  || |
Db        1099 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 1145

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
                | || |     ||  ||| |     |  ||  || || | ||| |    |  | | |
Db        1146 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1200

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
              |   |      |    ||  | | | ||     ||  | | |||          |  |
Db        1201 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1258

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
              | |    |  | |    ||||        |   | | | ||  |    |
Db        1259 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1318

Qy        1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
               |   | |||  |    |   ||| | |||          |     |  | ||
Db,       1319 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1368

Qy        1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
               || || || || || |||||||| |||| || ||||||||||||  ||||||  | |
Db        1369 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1428

Qy        1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
               | || || |      || ||      |||||||||||| || || || ||||  || ||||
Db        1429 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1488

Qy        1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
               |  | || ||| | ||| | ||  |  | || || ||| | |||||  |||| | ||
Db        1489 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1548

Qy        1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
               |||| |||| |||||   || || ||  |||| ||||||   ||    |  |  |
Db        1549 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1608

Qy        1312 CCCCATTTGTTACACAAGT 1330
                 || ||| |    ||| |
Db        1609 AGCCTTTTATGGACCAATT 1627
```

```
RESULT 12
AAL47323
ID   AAL47323 standard; DNA; 2764 BP.
XX
AC   AAL47323;
XX
DT   02-SEP-2002  (first entry)
XX
DE   Presenilin coding sequence.
XX
KW   Sel-12; presenilin; neuronal disorder; familial Alzheimer's disease;
KW   amyloid precursor protein; APP; ds.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             249..1652
FT                   /*tag=  a
FT                   /product= "presenilin"
XX
PN   US6376239-B1.
XX
PD   23-APR-2002.
XX
PF   04-APR-1997;   97US-0832867.
XX
PR   04-APR-1997;   97US-0832867.
XX
PA   (ELEG-) ELEGENE GMBH.
XX
PI   Baumeister R;
XX
DR   WPI; 2002-478281/51.
DR   P-PSDB; AAO18049.
XX
PT   Isolated DNA molecule comprising promoter of the sel-12 gene from
PT   Caenorhabditis elegans operably linked to heterologous gene, directs
PT   expression in neural cells and is useful to develop drugs to treat
PT   neuronal disorders  -
XX
PS   Claim 2; Fig 4; 78pp; English.
XX
CC   The present invention relates to DNA molecules comprising the promoter of
CC   the sel-12 gene from Caenorhabditis elegans operably linked to a
CC   heterologous DNA sequence encoding a protein of interest. The sequence
CC   can be used to develop drugs for the treatment, prevention or delay of a
CC   neuronal disorder. In particular, the neuronal disorder may be familial
CC   Alzheimer's disease. The present sequence is a presenilin coding sequence
CC   described in the exemplification of the invention.
XX
SQ   Sequence 2764 BP; 715 A; 624 C; 652 G; 773 T; 0 other;

  Query Match           16.5%;  Score 248.2;  DB 24;  Length 2764;
  Best Local Similarity   54.6%;  Pred. No. 3.8e-47;
  Matches  666;  Conservative    0;  Mismatches  513;  Indels   40;  Gaps    7;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||   |    ||||||| || ||    || || ||    |
Db        442 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 501

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | |||||| || ||| | || |||||||   |||| ||   ||| || ||  |  | |  |
Db        502 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 561

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
              ||||||  |  ||  |||   |||| || | |     || ||        || || || |
Db        562 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 618

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
              | | |  |||  |  ||  ||| ||  ||||||  | ||||| |  | ||  | |
Db        619 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 678

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
              || | |||||  | || ||| | ||| | ||||||||||| ||  |||||| | || ||||
Db        679 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 738

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
              |||||||||| |      | |  |  | || ||| | ||  |    || ||  ||   |
Db        739 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 798

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
              ||||  | ||||  |   | ||  ||     |    |   |||    |      | | |
Db        799 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 858

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
              | | ||| ||  | |||||||| |  || || ||||||||||| | || || || |||
Db        859 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 918

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
              || || ||||  ||   ||| || ||||| ||||| ||||||||||||| || ||||
Db        919 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 978

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
              |||||| |||| |  |  ||  ||| || || || |  ||| | || || ||  |    |
Db        979 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1038

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
              | ||||| ||| |  |      |||| ||||| || ||||||||||| ||  |  |||| |
Db        1039 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1098

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
              | || || ||||| || ||   | |              | | | ||| || |  ||  |
Db        1099 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 1145

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
                | || |     ||  ||| |       |  ||  || || | ||| |    |  | | |
Db        1146 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1200

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
              |    |     |    ||  | | | ||     ||  | | |||          |  |
Db        1201 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1258

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
              | |     |  | |     ||||        |    |  | | ||  |      |
Db        1259 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1318

Qy        1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
               |   | |||  |     |    ||| | |||            |      | | ||
Db        1319 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1368

Qy        1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
               || || || || || |||||||||  |||| || ||||||||||||  ||||||  | |
Db        1369 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1428

Qy        1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
               | || || |      || |        |||||||||||| || || || ||||  || ||||
Db        1429 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1488

Qy        1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
               |  | || ||| | ||| | ||  |  | || || ||| | |||||   |||| | || |
Db        1489 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1548

Qy        1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
               |||| |||| |||||   ||  || ||  |||| ||||||   ||    |  |  |
Db        1549 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1608

Qy        1312 CCCCATTTGTTACACAAGT 1330
               || ||| |    ||| |
Db        1609 AGCCTTTTATGGACCAATT 1627


RESULT 13
AAT40028
ID   AAT40028 standard; DNA; 2765 BP.
XX
```

```
AC   AAT40028;
XX
DT   22-JUL-1997  (first entry)
XX
DE   Presenilin-1-1 wild type coding sequence.
XX
KW   Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW   familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW   depression; antibody; gene expression modulator; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             249..1652
FT                   /*tag= a
FT                   /product= presenilin-1-1
XX
PN   WO9634099-A2.
XX
PD   31-OCT-1996.
XX
PF   29-APR-1996;    96WO-CA00263.
XX
PR   31-JUL-1995;    95US-0509359.
PR   28-APR-1995;    95US-0431048.
PR   28-JUN-1995;    95US-0496841.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1996-497631/49.
DR   P-PSDB; AAW05733.
XX
PT   New presenilin genes - useful for diagnosis, therapy and drug
PT   screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS   Claim 8; Page 128-130; 178pp; English.
XX
CC   AAT40028 and AAT40029 represent the coding sequences for the two
CC   different forms of wild type human presenilin-1 (PS-1). The form
CC   represented by AAT40029 results from alternate splicing of the genomic
CC   DNA sequence. AAT40031 represents the coding sequence for wild type human
CC   PS-2. The presenilins are a family of highly conserved integral membrane
CC   proteins with a common structural motif, common alternate splicing
CC   patterns, and common mutational hot spot regions. Mutations in PS genes
CC   are implicated in familial Alzheimer's disease (AD) and possibly other
CC   diseases such as cerebral haemorrhage, schizophrenia, depression etc., so
CC   detection of mutations in these sequences can be used for diagnosis of
CC   these diseases. The encoded proteins, or vectors that express them or
CC   containing antisense sequences, antibodies selective for mutant forms of
CC   the encoded proteins (such as AAW05736) and modulators of PS gene
CC   expression are potentially useful for treatment of AD etc. Transgenic
CC   animals are useful as models for drug screening. The antibodies can also
CC   be used e.g. for affinity purification and in immunoassays.
XX
SQ   Sequence 2765 BP; 715 A; 624 C; 652 G; 773 T; 1 other;

  Query Match           16.5%;  Score 248.2;  DB 17;  Length 2765;
  Best Local Similarity  54.6%;  Pred. No. 3.8e-47;
  Matches  666;  Conservative    0;  Mismatches  513;  Indels   40;  Gaps    7;

Qy       119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db       442 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 501

Qy       179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db       502 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 561

Qy       239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
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Db       562 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 618

Qy       299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db       619 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 678

Qy       359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db       679 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 738

Qy       419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db       739 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 798

Qy       479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db       799 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 858

Qy       539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db       859 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 918

Qy       599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db       919 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 978

Qy       659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db       979 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1038

Qy       719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db      1039 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1098

Qy       779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db      1099 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1145

Qy       839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db      1146 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1200

Qy       899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db      1201 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1258

Qy       959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db      1259 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1318

Qy      1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db      1319 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1368

Qy      1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db      1369 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1428

Qy      1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db      1429 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1488

Qy      1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db      1489 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1548

Qy      1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db      1549 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1608

Qy      1312 CCCCATTTGTTACACAAGT 1330
Db      1609 AGCCTTTTATGGACCAATT 1627
```

```
RESULT 14
AAT85332
ID   AAT85332 standard; DNA; 2765 BP.
XX
AC   AAT85332;
XX
DT   09-DEC-1997  (first entry)
XX
DE   Human S182 gene, PS1 locus, related to Alzheimer's disease.
XX
KW   Mutant; antisense; antibody; vaccine; Alzheimer's disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             249..1652
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FT                   /product= PS1
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FT                   /*tag= b
FT                   /note= "A mutated form of PS1 has c replacing the
FT                   wild-type t at this position"
FT   mutation        1039
FT                   /*tag= c
FT                   /note= "A mutated form of PS1 has t replacing the
FT                   wild-type c at this position"
FT   mutation        1054
FT                   /*tag= d
FT                   /note= "A mutated form of PS1 has a replacing the
FT                   wild-type g at this position"
XX
PN   WO9708319-A1.
XX
PD   06-MAR-1997.
XX
PF   03-SEP-1996;   96WO-US14114.
XX
PR   30-AUG-1996;   96US-0706344.
PR   31-AUG-1995;   95US-0003054.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Tanzi RE,  Wasco W;
XX
DR   WPI; 1997-179276/16.
DR   P-PSDB; AAW27176.
XX
PT   Chromosome 14 early-onset familial Alzheimer's disease gene PS1
PT   mutants - useful for diagnosing likelihood of developing Alzheimer's
PT   disease, also anti-sense sequences, antibodies and vaccines to delay
PT   onset
XX
PS   Disclosure; Page 69-72; 99pp; English.
XX
CC   The present sequence represents the human S182 gene, PS1 locus. Mutant
CC   PS1 produces a gene product that increases the probability of
CC   Alzheimer's disease. Possible mutations of the PS1 locus are shown in
CC   the features table. A nucleic acid sequence able to hybridise to
CC   sequences coding for a mutant PS1 polypeptide can be used as probes for
CC   diagnosing an increased likelihood of contracting Alzheimer's disease.
CC   Antibodies against the mutant polypeptide can also be used for this
CC   purpose. Vectors containing or expressing a nucleic acid molecule,
CC   protein or antibody specific for mutant PS1 can be administered to a
CC   patient to reduce the likelihood, or delay the onset, of Alzheimer's
CC   disease, e.g. anti-sense RNA expression can be used to decrease
CC   expression of the PS1 peptide. Transgenic animals expressing the
CC   Alzheimer's disease protein can be used to test candidate therapeutics
CC   and to investigate the normal role of PS1. The PS1 peptide may also be
CC   included in pharmaceutical compositions (vaccines) for Alzheimer's
CC   disease therapy.
XX
SQ   Sequence 2765 BP; 715 A; 625 C; 652 G; 772 T; 1 other;

  Query Match           16.5%;  Score 248.2;  DB 18;  Length 2765;
  Best Local Similarity  54.6%;  Pred. No. 3.8e-47;
  Matches  666;  Conservative    0;  Mismatches  513;  Indels   40;  Gaps    7;

Qy       119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db       442 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 501

Qy       179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db       502 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 561

Qy       239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db       562 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 618

Qy       299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db       619 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 678

Qy       359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db       679 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 738

Qy       419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db       739 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 798

Qy       479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db       799 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 858

Qy       539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db       859 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 918

Qy       599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db       919 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 978

Qy       659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db       979 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1038

Qy       719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db       1039 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1098

Qy       779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db       1099 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1145

Qy       839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db       1146 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGCATAATGCAG 1200

Qy       899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db       1201 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1258

Qy       959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db       1259 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1318

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db       1319 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1368

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db       1369 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1428
```

```
Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
              | || || |      || |       ||||||||||| || || || ||||  || ||||
Db       1429 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1488

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
              |  | || ||| | ||| | ||  |  | || || ||| | |||||   |||| | || |
Db       1489 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1548

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
              ||||  |||| |||||   ||  || ||  |||| ||||||   ||    |   |  |
Db       1549 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1608

Qy       1312 CCCCATTTGTTACACAAGT 1330
                || ||| |    ||| |
Db       1609 AGCCTTTTATGGACCAATT 1627
```

RESULT 15
AAV04666
ID AAV04666 standard; cDNA; 2765 BP.
XX
AC AAV04666;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human presenilin-1 cDNA (hPS1-1).
XX
KW Presenilin-1; PS1 gene; human; familial Alzheimer's disease; FAD;
KW cerebral haemorrhage; schizophrenia; depression; epilepsy;
KW mental retardation; diagnosis; therapy; transgenic animal; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
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FT	exon	1..113
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FT		/number= 1
FT	exon	114..195
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FT		/number= 4
FT	exon	336..586
FT		/*tag= e
FT		/number= 5
FT	exon	587..728
FT		/*tag= f
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FT	exon	729..796
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FT	exon	797..1017
FT		/*tag= h
FT		/number= 8
FT	exon	1018..1116
FT		/*tag= i
FT		/number= 9
FT	exon	1117..1203
FT		/*tag= j
FT		/number= 10
FT	exon	1204..1377
FT		/*tag= k
FT		/number= 11
FT	exon	1378..1496
FT		/*tag= l
FT		/number= 12
FT	exon	1497..2765
FT		/*tag= m
FT		/number= 13
FT	variation	324..335
FT		/*tag= n
FT		/note= "deletion of 12 nucleotides from 3' end of exon 4 by alternative splicing, deletes Val26-Gln-29 (not critical to PS1 function)"
FT	variation	1018..1116
FT		/*tag= o
FT		/note= "absence of exon 9 through splicing variation, results in Asp-257 changing to Ala and fusion of Ala-257 to Thr-291"
FT	mutation	492
FT		/*tag= p
FT		/note= "G to C FAD mutation site (Val82Leu)"
FT	mutation	591
FT		/*tag= q
FT		/note= "T to C FAD mutation site (Tyr115His)"
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FT		/*tag= r
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FT		/*tag= s
FT		/note= "T to C FAD mutation site (Ile143Thr)"
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FT		/note= "A to C FAD mutation site (Met146Leu)"
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FT		/note= "A to G FAD mutation site (His163Arg)"
FT	mutation	939
FT		/*tag= v
FT		/note= "G to A FAD mutation site (Ala231Thr)"
FT	mutation	985
FT		/*tag= w
FT		/note= "C to A FAD mutation site (Ala246Glu)"
FT	mutation	1027
FT		/*tag= x
FT		/note= "C to T FAD mutation site (Ala260Val)"
FT	mutation	1039
FT		/*tag= y
FT		/note= "C to T FAD mutation site (Pro264Leu)"
FT	mutation	1192
FT		/*tag= z
FT		/note= "C to T FAD mutation site (Ala285Val)"
FT	mutation	1104
FT		/*tag= aa
FT		/note= "C to G FAD mutation site (Leu286Val)"
FT	mutation	1399
FT		/*tag= ab
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FT		/*tag= ac
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FT		/note= "G to A FAD mutation site (Cys410Tyr)"
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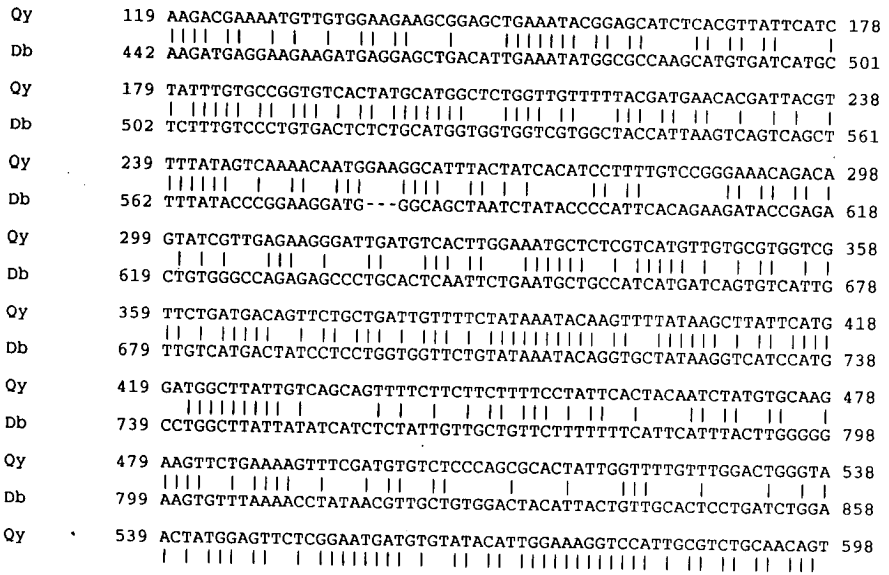
FT		/*tag= ae
FT		/note= "A to G FAD mutation site (Ile439Val)"

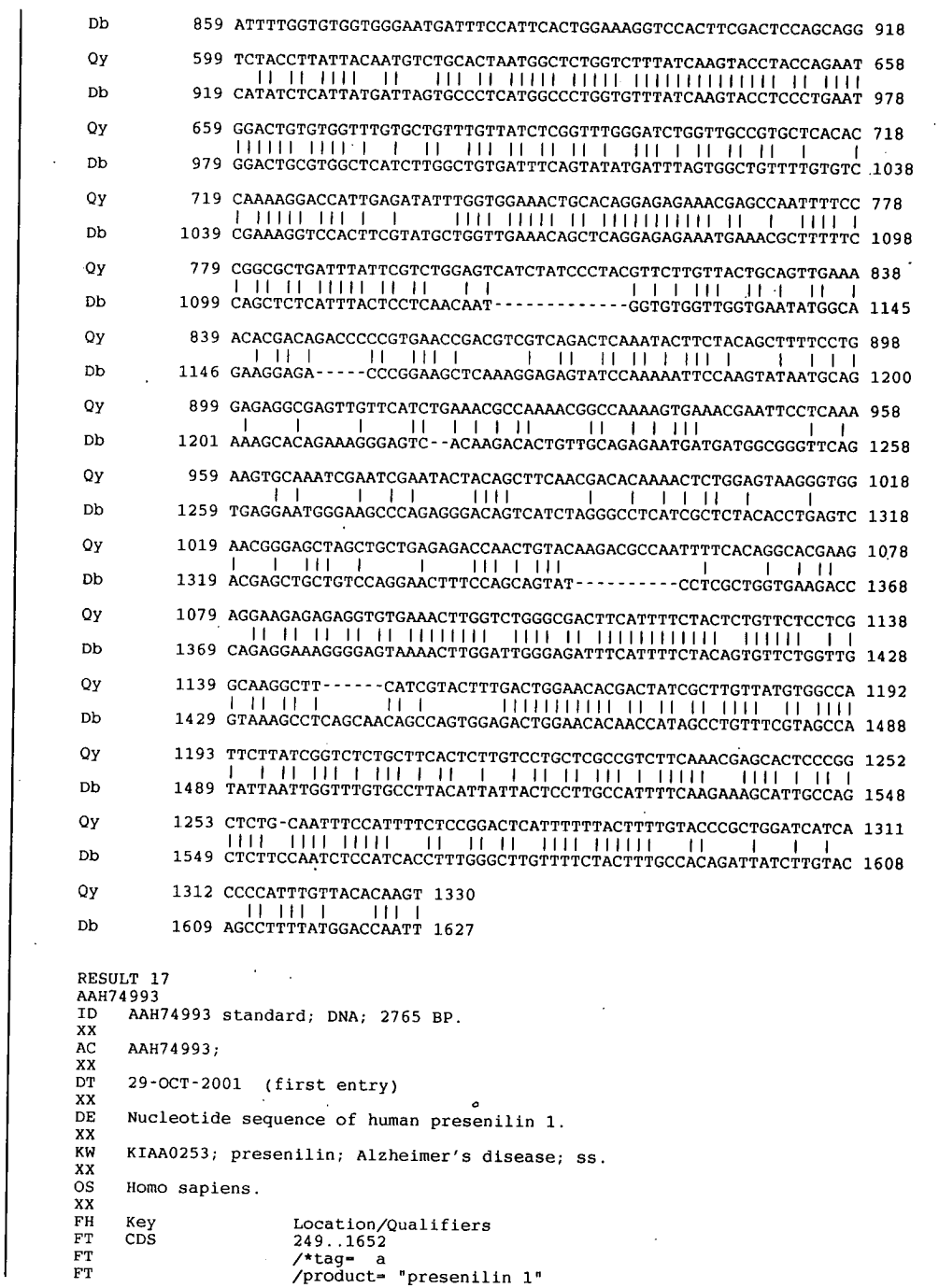
XX
PN WO9801549-A2.
XX
PD 15-JAN-1998.
XX
PF 04-JUL-1997; 97WO-CA00475.
XX
PR 02-JAN-1997; 97US-0034590.
PR 05-JUL-1996; 96US-0021673.
PR 12-JUL-1996; 96US-0021700.
PR 08-NOV-1996; 96US-0029895.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.

```
XX
PI   Fraser PE, Rommens JM, St George-Hyslop PH;
XX
DR   WPI; 1998-286355/25.
DR   P-PSDB; AAW23964.
XX
PT   New isolated mutant presenilin-1 genes - useful for developing
PT   products for use in detection, diagnosis and therapy of Alzheimer's
PT   disease and for drug screening
XX
PS   Disclosure; Page 178-180; 238pp; English.
XX
CC   This cDNA clone, deposited as ATCC 97124, codes for human
CC   presenilin-1 (hPS1, see AAW23964). Mutations in the presenilin genes
CC   have been linked to the development in humans of forms of familial
CC   Alzheimer's disease (FAD) and may be causative of other disorders,
CC   e.g. cognitive, intellectual, neurological or physiological
CC   disorders such as cerebral haemorrhage, schizophrenia, depression,
CC   mental retardation and epilepsy. Isolation of the hPS1 cDNA
CC   followed genetic mapping of the AD3 region at 14q24.3, construction
CC   of a physical contig spanning the AD3 region, transcription mapping
CC   and analysis of candidate genes, and recovery of candidate genes by
CC   RT-PCR from brain mRNA. In this cDNA, exon 1 is spliced directly
CC   to exon 3. Other hPS1 sequences (see also AAV04667) result from
CC   alternative splicing of the mRNA transcript. A mouse PS1 homologue
CC   (see AAV04668) and a human presenilin-2 sequence (see AAV04669) are
CC   also provided, as well as genomic sequences for hPS1 (see
CC   AAT99661-71). Use of the nucleic acids and proteins comprising or
CC   derived from the presenilins is made in screening and diagnosing
CC   FAD, identifying and developing therapeutics for treatment of FAD,
CC   and in producing cell lines and transgenic animals useful as models
CC   of FAD. Nucleic acids (see AAV04674-80) encoding presenilin
CC   interacting proteins are also provided.
XX
SQ   Sequence 2765 BP; 715 A; 624 C; 652 G; 773 T; 1 other;

  Query Match            16.5%;  Score 248.2;  DB 19;  Length 2765;
  Best Local Similarity  54.6%;  Pred. No. 3.8e-47;
  Matches  666;  Conservative    0;  Mismatches  513;  Indels   40;  Gaps    7;

Qy       119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db       442 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 501

Qy       179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db       502 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 561

Qy       239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db       562 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 618

Qy       299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db       619 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 678

Qy       359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db       679 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 738

Qy       419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db       739 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 798

Qy       479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db       799 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 858

Qy       539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db       859 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 918

Qy       599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db       919 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 978

Qy       659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db       979 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1038

Qy       719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db       1039 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1098

Qy       779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db       1099 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1145

Qy       839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db       1146 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1200

Qy       899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db       1201 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1258

Qy       959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db       1259 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1318

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db       1319 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1368

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db       1369 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1428

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db       1429 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1488

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db       1489 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1548

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db       1549 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1608

Qy.      1312 CCCCATTTGTTACACAAGT 1330
Db       1609 AGCCTTTTATGGACCAATT 1627


RESULT 16
AAD18120
ID   AAD18120 standard; DNA; 2765 BP.
XX
AC   AAD18120;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human presenilin-1 (PS-1) protein DNA.
XX
KW   Human; catenin p120; presenilin-1; PS-1; neuroprotective; gene therapy;
KW   neurodegenerative disease; Alzheimer's disease; nootropic; prophylaxis;
KW   neuronal disorder; cognitive disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             249..1652
FT                   /*tag= a
FT                   /product= "Human presenilin-1 protein"
XX
```

PN WO200167097-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-GB01059.
XX
PR 10-MAR-2000; 2000GB-0005895.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Hale RS, Rowley A, Blackstock W;
XX
DR WPI; 2001-589954/66.
DR P-PSDB; AAE10798.
XX
PT Identifying presenilin or catenin p120 activity modulator useful for
PT modulating presenilin-catenin p120 interaction and thus for treating
PT cognitive disorder e.g., Alzheimer's disease comprises enhancing
PT cognitive function -
XX
PS Example 1; Page 43-45; 48pp; English.
XX
CC The invention relates to a method for identifying modulators of
CC presenilin and catenin p120. Modulators of catenin p120 and presenilin
CC are useful for the treatment and prophylaxis of disorders that is
CC responsive to modulation of presenilin/catenin p120 activity. In
CC particular, neuronal disorders such as cognitive disorders and
CC neurodegenerative diseases such as Alzheimer's disease. Catenin p120 DNAs
CC are useful for identifying mutations in catenin p120 genes.
CC Identification of such mutations assist in the diagnosis of or
CC susceptibility to Alzheimer's or other conditions associated with
CC presenilin and in assessing the physiology of such disorders. Catenin
CC p120 DNAs are also used in hybridisation studies to monitor expression of
CC p120 genes and in particular for up or down regulation of catenin p120
CC expression. The present DNA sequence encodes human presenilin-1 (PS-1)
CC protein.
XX
SQ Sequence 2765 BP; 715 A; 624 C; 652 G; 773 T; 1 other;

Query Match 16.5%; Score 248.2; DB 22; Length 2765;
Best Local Similarity 54.6%; Pred. No. 3.8e-47;
Matches 666; Conservative 0; Mismatches 513; Indels 40; Gaps 7;





RESULT 17
AAH74993
ID AAH74993 standard; DNA; 2765 BP.
XX
AC AAH74993;
XX
DT 29-OCT-2001 (first entry)
XX
DE Nucleotide sequence of human presenilin 1.
XX
KW KIAA0253; presenilin; Alzheimer's disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 249..1652
FT /*tag= a
FT /product= "presenilin 1"

XX
PN WO200167109-A1.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-GB01057.
XX
PR 10-MAR-2000; 2000GB-0005894.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Hale RS, Rowley A, Blackstock W;
XX
DR WPI; 2001-522960/57.
DR P-PSDB; AAG63936.
XX
PT Identifying a modulator of presenilin function by determining the
PT ability of presenilin to bind to a K1AA0253 polypeptide in the presence
PT and absence of a test compound, useful in the treatment or prophylaxis
PT of Alzheimer's disease -
XX
PS Disclosure; Page 42-44; 48pp; English.
XX
CC The present sequence encodes human presenilin 1. KIAA0253 binds to
CC presenilin. The specification describes a method of identifying a
CC modulator of presenilin function or KIAA0253 function. The method
CC comprises determining presenilin activity or KIAA0253 activity
CC in the presence and absence of a test compound, where presenilin
CC activity is determined by its ability to bind to KIAA0253. A modulator
CC of presenilin or K1AA0253 polypeptide is useful in the manufacture of
CC a medicament for the treatment or prophylaxis of Alzheimer's disease.
CC The K1AA0253 polynucleotide and K1AA0253 polypeptide are useful in the
CC treatment, prophylaxis or diagnosis of Alzheimer's disease.
XX
SQ Sequence 2765 BP; 715 A; 624 C; 652 G; 773 T; 1 other;

Query Match 16.5%; Score 248.2; DB 22; Length 2765;
Best Local Similarity 54.6%; Pred. No. 3.8e-47;
Matches 666; Conservative 0; Mismatches 513; Indels 40; Gaps 7;

```
Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||    |    ||||||| || ||    || || ||    |
Db        442 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 501

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | ||||| || ||| | || |||||||   |||| ||   ||| || ||  |  | |  |
Db        502 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 561

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
              ||||||  |  ||  |||   ||||  || | |     || ||       || || || |
Db        562 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 618

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
                | |  |   |||  |   ||   ||| ||   ||||||  | ||||| |  | ||  | |
Db        619 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 678

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
              || | |||||  | || ||| | ||| | ||||||||||  ||  ||||||  | || ||||
Db        679 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 738

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
                |||||||||  |      | |  |  | || ||| | ||  |    || ||  ||   |
Db        739 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 798

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
              ||||  | ||||  |   | ||  ||     |    |   |||    |     |  | |
Db        799 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 858

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
              | | ||| ||  | |||||||| |  || || ||||||||||| | || || || |||
Db        859 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 918

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
```

```
                || || ||||  ||   ||| || ||||| ||||| ||||||||||||| || ||||
Db        919 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 978

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
              |||||| |||| |  |  ||  ||| || || || |  ||| | || || ||  |    |
Db        979 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1038

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
              | |||||| ||| |  |     |||| ||||| || ||||||||||| ||  |  |||| |
Db        1039 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1098

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
              | || || ||||| || ||   | |             | | | |||  || |  ||  |
Db        1099 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1145

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
                | || |      ||  ||| |      |  ||  || || | ||| |    |  | | |
Db        1146 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1200

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
                |    |     | . ||  | | | ||     ||  | | |||         |  |
Db        1201 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1258

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
                | |     |  | |     ||||       |   |  | | ||  |     |
Db        1259 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1318

Qy        1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
               |   |  |||  |     |    ||| | |||                |     | | ||
Db        1319 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1368

Qy        1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
                || || || || ||  |||||||  |||| || ||||||||||||  |||||  | |
Db        1369 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1428

Qy        1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
                | || || |       || |        |||||||||| || || || ||||  || ||||
Db        1429 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1488

Qy        1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
               |  | || ||| | ||| | ||  |  | || || ||| | |||||   |||| | || |
Db        1489 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1548

Qy        1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
                |||| |||| |||||   ||  || ||  |||| ||||||   ||     |  |  |
Db        1549 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1608

Qy        1312 CCCCATTTGTTACACAAGT 1330
                || ||| |    ||| |
Db        1609 AGCCTTTTATGGACCAATT 1627
```

RESULT 18
AAD27443
ID AAD27443 standard; cDNA; 1404 BP.
XX
AC AAD27443;
XX
DT 18-APR-2002 (first entry)
XX
DE Human mutant presenilin 1 (PS1) cDNA #1.
XX
KW Human; presenilin 1; PS1; amyloid precursor protein; APP; drug screening;
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
KW Huntington's disease; amylotrophic lateral sclerosis; Picks disease;
KW head injury disease; frontal lobe dementia; cerebellar degeneration;
KW ischaemic injury; schizophrenia; mutant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1404

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FT                  /*tag=  a
FT                  /product= "Human mutant presenilin-1 protein"
FT                  /transl_except= (pos:772..774, aa:Xaa)
FT                  /transl_except= (pos:775..777, aa:Xaa)
FT                  /note= "Xaa corresponds to unknown amino acid"
XX
PN   WO200202601-A2.
XX
PD   10-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US16508.
XX
PR   30-JUN-2000; 2000US-215345P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Carter DB,  Tomasselli AG;
XX
DR   WPI; 2002-140082/18.
DR   P-PSDB; AAE17045.
XX
PT   Novel isolated mutant presenilin 1 and presenilin 2 polypeptides,
PT   useful for screening of drugs for treating pathologies associated with
PT   aberrant amyloid precursor protein processing, such as Alzheimer's
PT   disease -
XX
PS   Claim 44; Page 65; 80pp; English.
XX
CC   The invention relates to mutant presenilin 1 (PS1) and presenilin 2
CC   (PS2) polypeptides. Presenilin are involved in the processing of amyloid
CC   precursor protein (APP) from which major amylodogenic peptides are
CC   cleaved. Mutant presenilins are useful for identifying agents that
CC   modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
CC   presenilin is also useful as a target for screening drugs useful in the
CC   treatment of pathologies associated with aberrant amyloid precursor
CC   protein processing, such as Alzheimer's disease, Parkinson's disease,
CC   multiple sclerosis, Huntington's disease, amylotrophic lateral sclerosis,
CC   head injury disease, Picks disease, frontal lobe dementia, cerebellar
CC   degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
CC   non-human animal is useful for analysing the interaction between APP and
CC   mutant presenilin-processing protease in vivo, and for screening anti-
CC   Alzheimer's disease drugs in vivo. The present sequence is human
CC   mutant PS1 cDNA.
XX
SQ   Sequence 1404 BP; 361 A; 312 C; 335 G; 390 T; 6 other;

  Query Match             16.5%;  Score 247;  DB 24;  Length 1404;
  Best Local Similarity   54.4%;  Pred. No. 5.9e-47;
  Matches  663;  Conservative    0;  Mismatches  516;  Indels   40;  Gaps    7;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||   |    ||||||| || ||   || || ||   |
Db        194 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 253

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | ||||| || ||| | || |||||||   |||| ||   ||| || ||  |  | |  |
Db        254 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 313

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
              ||||||  |  ||  |||   ||||  || | |     || ||       || || || |
Db        314 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 370

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
              | | |   |||  |   ||   ||| ||  ||||||  | ||||| |  | ||  | |
Db        371 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 430

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
              || | |||||  | || ||| | ||| | |||||||||| ||  ||||||  | || ||||
Db        431 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 490

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
              |||||||||  |      | |  |  | || ||| | ||  |    || ||  ||   |
Db        491 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 550

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
              ||||  |  |||| |   | ||  ||      |   |   |||    |      |  | |
Db        551 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 610

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
              | | ||| ||  | |||||||| |  || || ||||||||||||| | || || || |||
Db        611 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 670

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
                || || ||||  ||   ||| || ||||| ||||| |||||||||||||| || ||||
Db        671 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 730

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
              ||||||| |||| |  |  ||  ||| || || || |  |||      || ||  |    |
Db        731 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATNNNNNNGCTGTTTTGTGTC 790

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
              | ||||| ||| |  |     |||| ||||| || ||||||||||| ||  |  |||| |
Db        791 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 850

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
              | || || ||||| || ||  | |                | | | |||  || |  ||  |
Db        851 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 897

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
              | || |     ||  ||| |       |  ||  || || || |  |||  |    | | | |
Db        898 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 952

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
              |    |     |    ||  | | | ||     ||  | | |||          |  |
Db        953 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1010

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
                | |     |  | |     ||||     |   |  | | ||  |     |
Db       1011 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1070

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
              |   |  |||  |      |    ||| | |||             |     |  | ||
Db       1071 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1120

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
                || || || || || ||||||||  |||| || ||||||||||||  ||||||  | |
Db       1121 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1180

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
              | || || |      || |       ||||||||||| || || || ||||  || ||||
Db       1181 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1240

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
              |  | || ||| | ||| | ||  |  | || || ||| | |||||   |||| | || |
Db       1241 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1300

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
              ||||  |||| |||||   ||  || ||  |||| ||||||   ||    |  | |
Db       1301 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1360

Qy       1312 CCCCATTTGTTACACAAGT 1330
                || ||| |   ||| |
Db       1361 AGCCTTTTATGGACCAATT 1379


RESULT 19
AAT63207
ID   AAT63207 standard; cDNA; 1911 BP.
XX
AC   AAT63207;
XX
DT   17-JUN-1997  (first entry)
XX
DE   Human S182 gene associated with familial Alzheimer's disease.
XX
KW   S182 gene; familial Alzheimer's disease; diagnosis;
```

```
KW   transgenic animal; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             220..1611
FT                   /*tag= a
XX
PN   WO9703999-A1.
XX
PD   06-FEB-1997.
XX
PF   26-JUN-1996;    96WO-US11065.
XX
PR   02-AUG-1995;    95US-0001800.
PR   18-JUL-1995;    95US-0001500.
XX
PA   (UYSF-) UNIV SOUTH FLORIDA.
PA   (UNIW ) UNIV WASHINGTON SCHOOL MED.
XX
PI   Goate AM,  Hardy JA;
XX
DR   WPI; 1997-132571/12.
DR   P-PSDB; AAW12376.
XX
PT   New mutants of the S182 gene associated with familial Alzheimer's
PT   disease - and related protein and transgenic animals, useful as
PT   models for screening and assessing potential drugs
XX
PS   Disclosure; Fig 1A-D; 26pp; English.
XX
CC   An S182 gene cDNA clone (AAT63207), deposited as ATCC 97238, was
CC   isolated from a human brain library.  Several mutations in the S182
CC   gene have been found in families with members affected by early
CC   onset Alzheimer's disease (AD): in 2 families Met to Val at codon
CC   135; in 3 families Met to Val at 142; in 1 family Pro to Ser at 263;
CC   in 4 families Glu to Ala at 276; and in 1 family Glu to Gly at 280.
CC   In all cases the mutations were detected only in affected family
CC   members.  Detection of the mutations, e.g. by PCR (see also AAT63208-
CC   13), is used to diagnose AD, or a predisposition to it.  Transgenic
CC   animals can be produced, useful as models for screening and
CC   assessing potential drugs.  Probes based on the gene can be used to
CC   identify homologues of S182, e.g. one present on human chromosome 1
CC   which may be associated with AD in some families.
XX
SQ   Sequence 1911 BP; 491 A; 428 C; 465 G; 519 T; 8 other;

  Query Match            16.4%;  Score 246.6;  DB 18;  Length 1911;
  Best Local Similarity  54.6%;  Pred. No. 7.9e-47;
  Matches  665;  Conservative    0;  Mismatches  514;  Indels   40;  Gaps    7;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||   |    ||||||| || ||    || || ||   |
Db        401 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 460

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | ||||| || ||| | || |||||||   |||| ||   ||| || ||  |  | |  |
Db        461 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 520

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
              ||||||  |  ||  |||   ||||  || | |     || ||        || || || |
Db        521 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 577

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
                | | |   |||  |   ||  ||| ||   ||||||  | |||||  |  | ||  | |
Db        578 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 637

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
              || | |||||  | || ||| | ||| | ||||||||||| ||  ||||||  | || ||||
Db        638 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 697

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
                |||||||||  |      | |  |  | || ||| | ||  |    || ||  ||   |

Db        698 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 757

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
              ||||  | ||||  |   | ||  ||      |   |   |||    |    |  | |
Db        758 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 817

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
              | | ||| ||  | |||||||| |  || || ||||||||||||| | || || || |||
Db        818 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 877

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
                || || ||||  ||   ||| || ||||| ||||| ||||||||||||| || ||||
Db        878 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 937

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
              |||||| |||| |  |  ||  ||| || || || |  ||| | || || ||  |    |
Db        938 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 997

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
              | ||||| ||| |  |      |||| ||||| || ||||||||| | ||  |  |||| |
Db        998 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAGATGAAACGCTTTTTC 1057

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
              | || || ||||| || ||   | |             | | | |||  || |  ||  |
Db       1058 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 1104

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
                | || |     ||  ||| |      |  ||  || || | ||| |    |  | | |
Db       1105 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1159

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
              |    |     |    ||  | | ||     ||  | | |||           |  |
Db       1160 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1217

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
                | |     |  | |     ||||       |   |  | | ||  |     |
Db       1218 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1277

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
              |   |  ||| |     |   ||| | ||          |   |    | | ||
Db       1278 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGT----------ATCCTCGCTGGTGAAGACC 1327

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
                || || ||  || || |||||||  |||| || ||||||||||||  ||||||  | |
Db       1328 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1387

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
              | || || |      || |       |||||||||||| || || || ||||  || ||||
Db       1388 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1447

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
              |  | || ||| | ||| | ||  |  | || || ||| | |||||   |||| | || |
Db       1448 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1507

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
              ||||  |||| ||||||   ||  || ||  |||| ||||||    ||     |  | |
Db       1508 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1567

Qy       1312 CCCCATTTGTTACACAAGT 1330
                || ||| |    ||| |
Db       1568 AGCCTTTTATGGACCAATT 1586


RESULT 20
AAT75576
ID   AAT75576 standard; cDNA; 1914 BP.
XX
AC   AAT75576;
XX
DT   19-MAR-1998  (first entry)
XX
DE   Presenilin-1 VRSQ variant gene.
XX
```

```
KW   Identification; determination; neurological disease susceptibility;
KW   detection; alternative splice site; polyadenylated mRNA transcript;
KW   familial Alzheimer's disease; FAD; presenilin 1; VRSQ variant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             220..1611
FT                   /*tag= a
XX
PN   EP791660-A1.
XX
PD   27-AUG-1997.
XX
PF   14-FEB-1997;   97EP-0300988.
XX
PR   22-FEB-1996;   96US-0012077.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (UYSF-) UNIV SOUTH FLORIDA DEPT PSYCHIATRY.
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Barton A, Goate A, Hardy J;
XX
DR   WPI; 1997-418049/39.
DR   P-PSDB; AAW22948.
XX
PT   Diagnosis of, or susceptibility to neurological disease -
PT   specifically Alzheimer's disease, by detecting aberrant splicing in
PT   mRNA
XX
PS   Example 1; Page 8; 21pp; English.
XX
CC   Identifying susceptibility to a neurological disease, comprises
CC   detecting an alternative splice site in a polyadenylated mRNA
CC   transcript in a sample of genetic material, where the alternative.
CC   splice site encodes AAW22944, or detecting AAW22944 in the protein
CC   encoded by the mRNA. Tests on 3 early onset familial Alzheimer's
CC   disease (FAD) patients, 6 late onset sporadic Alzheimer's disease
CC   (AD) patients and 4 neurologically normal subjects, indicated that
CC   mRNA transcripts of the presenilin 1 gene in samples from various
CC   brain regions occur in 2 forms, PS-1-long (containing a VRSQ
CC   motif) and PS-1-short (lacking the VRSQ motif, i.e. the protein
CC   encoded by the present sequence), and that the PS-1-long levels
CC   in hippocampus and frontal cortex samples are significantly lower
CC   in FAD patients than in AD and normal subjects.
XX
SQ   Sequence 1914 BP; 492 A; 427 C; 467 G; 520 T; 8 other;

  Query Match             16.4%;  Score 246.6;  DB 18;  Length 1914;
  Best Local Similarity   54.6%;  Pred. No. 7.9e-47;
  Matches  665;  Conservative    0;  Mismatches  514;  Indels   40;  Gaps    7;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||   |    ||||||| || ||    || || ||    |
Db        401 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 460

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | ||||| || ||| | || |||||||   |||| ||   ||| || ||  |  | |  |
Db        461 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 520

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
              ||||||  |  ||  |||   ||||  || | |     || ||       || || || |
Db        521 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 577

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
              | | |   |||  |   ||   ||| ||   ||||||  | ||||| |  | ||  | |
Db        578 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 637

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
              || | |||||  | || ||| | ||| | |||||||||| ||  |||||| | || ||||
Db        638 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 697

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
              |||||||||  |      | |  |  | || ||| | ||  |    || ||  ||   |
Db        698 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 757

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
              ||||  |  ||||  |   | ||  ||      |    |   |||  |      |  | |
Db        758 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 817

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
              | |  ||| ||  | |||||||| |  || || ||||||||||||| | || || || |||
Db        818 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 877

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
                || || |||  ||   ||| || ||||| ||||| ||||||||||||||| || ||||
Db        878 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 937

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
              |||||| |||| |  |  ||  ||| || || || |  ||| | || || ||  |    |
Db        938 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 997

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
              | ||||| ||| |  |     |||| ||||| || |||||||| | ||  |  |||| |
Db        998 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAGATGAAACGCTTTTTC 1057

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
              | || || ||||| || ||   | |              | | | |||  || |  ||  |
Db       1058 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 1104

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
              | || |     ||  ||| |       |  ||  || || | ||| |    |  | | | |
Db       1105 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1159

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
              |    |     |   ||  | | | ||     ||  | | |||          |  |
Db       1160 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1217

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
              | |    |  | |    ||||      |   |  | | ||  |     |
Db       1218 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1277

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
              |   |  |||  |     |   ||| | ||           |   |     |  | ||
Db       1278 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGT----------ATCCTCGCTGGTGAAGACC 1327

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
              || || || || || ||||||||  |||| || ||||||||||||  ||||||  | | |
Db       1328 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1387

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
              | || || |      ||  |      |||||||||||  || || || ||||  || ||||
Db       1388 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1447

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
              |  | || ||| | ||| | ||  |  | || || ||| | |||||  |||| | || |
Db       1448 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1507

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
              ||||  |||| |||||   ||  || ||  |||| ||||||   ||    |   | |
Db       1508 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1567

Qy       1312 CCCCATTTGTTACACAAGT 1330
              || ||| |    ||| |
Db       1568 AGCCTTTTATGGACCAATT 1586


RESULT 21
ABK83912
ID   ABK83912 standard; cDNA; 3056 BP.
XX
AC   ABK83912;
XX
DT   14-AUG-2002  (first entry)
XX
```

DE Human cDNA differentially expressed in granulocytic cells #483.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID No 483; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3056 BP; 762 A; 688 C; 740 G; 866 T; 0 other;

Query Match 16.4%; Score 246.6; DB 24; Length 3056;
Best Local Similarity 54.6%; Pred. No. 9.1e-47;
Matches 665; Conservative 0; Mismatches 514; Indels 40; Gaps 7;

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Qy       119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db       735 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 794

Qy       179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db       795 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 854

Qy       239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db       855 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 911

Qy       299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db       912 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 971

Qy       359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db       972 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 1031

Qy       419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db       1032 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 1091

Qy       479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db       1092 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 1151

Qy       539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db       1152 ATTTGGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 1211

Qy       599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db       1212 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 1271

Qy       659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db       1272 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1331

Qy       719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db       1332 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1391

Qy       779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db       1392 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1438

Qy       839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db       1439 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1493

Qy       899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db       1494 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1551

Qy       959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db       1552 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1611

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db       1612 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1661

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db       1662 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1721

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
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Db       1722 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1781

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252

Db       1782 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1841

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311

Db       1842 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1901

Qy       1312 CCCCATTTGTTACACAAGT 1330

Db       1902 AGCCTTTTATGGACCAATT 1920


RESULT 22
AAT40029
ID   AAT40029 standard; DNA; 3086 BP.
XX
AC   AAT40029;
XX
DT   23-JUL-1997  (first entry)
XX
DE   Presenilin-1-2, alternatively spliced coding sequence..
XX
KW   Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW   familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW   depression; antibody; gene expression modulator; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             547..1948
FT                   /*tag= a
FT                   /product= presenilin-1-2
XX
PN   WO9634099-A2.
XX
PD   31-OCT-1996.
XX
PF   29-APR-1996;    96WO-CA00263.
XX
PR   31-JUL-1995;    95US-0509359.
PR   28-APR-1995;    95US-0431048.
PR   28-JUN-1995;    95US-0496841.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1996-497631/49.
DR   P-PSDB; AAW05734.
XX
PT   New presenilin genes - useful for diagnosis, therapy and drug
PT   screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS   Claim 8; Page 132-134; 178pp; English.
XX
CC   AAT40028 and AAT40029 represent the coding sequences for the two
CC   different forms of wild type human presenilin-1 (PS-1). The form
CC   represented by this sequence results from alternate splicing of the
CC   genomic DNA. AAT40031 represents the coding sequence for wild type human
CC   PS-2. The presenilins are a family of highly conserved integral membrane
CC   proteins with a common structural motif, common alternate splicing
CC   patterns, and common mutational hot spot regions. Mutations in PS genes
CC   are implicated in familial Alzheimer's disease (AD) and possibly other
CC   diseases such as cerebral haemorrhage, schizophrenia, depression etc., so
CC   detection of mutations in these sequences can be used for diagnosis of
CC   these diseases. The encoded proteins, or vectors that express them or
CC   containing antisense sequences, antibodies selective for mutant forms of
CC   the encoded proteins (such as AAW05736) and modulators of PS gene
CC   expression are potentially useful for treatment of AD etc. Transgenic
CC   animals are useful as models for drug screening. The antibodies can also
CC   be used e.g. for affinity purification and in immunoassays.
XX
SQ   Sequence 3086 BP; 789 A; 688 C; 740 G; 866 T; 3 other;

  Query Match             16.4%;  Score 246.6;  DB 17;  Length 3086;
  Best Local Similarity   54.6%;  Pred. No. 9.1e-47;
  Matches  665;  Conservative    0;  Mismatches  514;  Indels   40;  Gaps    7;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178

Db        738 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 797

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238

Db        798 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 857

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298

Db        858 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 914

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358

Db        915 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 974

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418

Db        975 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 1034

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478

Db       1035 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 1094

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538

Db       1095 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 1154

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598

Db       1155 ATTTGGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 1214

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658

Db       1215 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 1274

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718

Db       1275 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1334

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778

Db       1335 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1394

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838

Db       1395 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1441

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898

Db       1442 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1496

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958

Db       1497 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1554

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018

Db       1555 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1614

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078

Db       1615 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1664
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Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db       1665 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1724

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db       1725 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1784

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db       1785 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1844

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db       1845 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1904

Qy       1312 CCCCATTTGTTACACAAGT 1330
Db       1905 AGCCTTTTATGGACCAATT 1923
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RESULT 23
AAV04667
ID   AAV04667 standard; cDNA; 3086 BP.
XX
AC   AAV04667;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human presenilin-1 cDNA (hPS1-2).
XX
KW   Presenilin-1; PS1 gene; human; familial Alzheimer's disease; FAD;
KW   cerebral haemorrhage; schizophrenia; depression; epilepsy;
KW   mental retardation; diagnosis; therapy; transgenic animal; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             557..1948
FT                   /*tag=  a
XX
PN   WO9801549-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-CA00475.
XX
PR   02-JAN-1997;   97US-0034590.
PR   05-JUL-1996;   96US-0021673.
PR   12-JUL-1996;   96US-0021700.
PR   08-NOV-1996;   96US-0029895.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1998-286355/25.
DR   P-PSDB; AAW23965.
XX
PT   New isolated mutant presenilin-1 genes - useful for developing
PT   products for use in detection, diagnosis and therapy of Alzheimer's
PT   disease and for drug screening
XX
PS   Disclosure; Page 182-185; 238pp; English.
XX
CC   This cDNA clone, deposited as ATCC 97508, codes for human
CC   presenilin-1 (hPS1, see AAW23965).  Mutations in the presenilin genes
CC   have been linked to the development in humans of forms of familial
CC   Alzheimer's disease (FAD) and may be causative of other disorders,
CC   e.g. cognitive, intellectual, neurological or physiological
CC   disorders such as cerebral haemorrhage, schizophrenia, depression,
CC   mental retardation and epilepsy.  In this cDNA, exon 2 is the
CC   the initial exon.  Another, more prevalent hPS1 sequence (see
CC   AAV04666) results from alternative splicing of the mRNA transcript
CC   in which exon 1 is directly spliced to exon 3.  A mouse PS1
CC   homologue (see AAV04668) and a human presenilin-2 sequence (see
CC   AAV04669) are also provided, as well as genomic sequences for the
CC   hPS1 gene (see AAT99661-71).  Use of the nucleic acids and proteins
CC   comprising or derived from the presenilins is made in screening and
CC   diagnosing FAD, identifying and developing therapeutics for
CC   treatment of FAD, and in producing cell lines and transgenic
CC   animals useful as models of FAD.  Nucleic acids (see AAV04674-80)
CC   encoding presenilin interacting proteins are also provided.
XX
SQ   Sequence 3086 BP; 789 A; 688 C; 740 G; 866 T; 3 other;
```

```
  Query Match           16.4%;  Score 246.6;  DB 19;  Length 3086;
  Best Local Similarity  54.6%;  Pred. No. 9.1e-47;
  Matches  665;  Conservative    0;  Mismatches  514;  Indels   40;  Gaps    7;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db        738 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 797

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db        798 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 857

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db        858 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 914

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db        915 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 974

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db        975 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 1034

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db       1035 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 1094

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db       1095 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 1154

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db       1155 ATTTGGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 1214

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db       1215 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 1274

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db       1275 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 1334

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db       1335 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1394

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db       1395 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1441

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db       1442 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1496

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
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Db       1497 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1554

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018

Db       1555 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1614

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078

Db       1615 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1664

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138

Db       1665 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1724

Qy       1139 GCAAGGCTT------CATCGTACTTTGACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192

Db       1725 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1784

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252

Db       1785 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1844

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311

Db       1845 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1904

Qy       1312 CCCCATTTGTTACACAAGT 1330

Db       1905 AGCCTTTTATGGACCAATT 1923
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RESULT 24
AAV03246
ID AAV03246 standard; cDNA; 1750 BP.
XX
AC AAV03246;
XX
DT 08-JUN-1998 (first entry)
XX
DE Human presenilin I cDNA.
XX
KW Presenilin I gene; familial adult onset Alzheimer's disease; FAD;
KW diagnosis; human; VRXQ motif; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 174..1565
FT /*tag= a
XX
PN EP814157-A2.
XX
PD 29-DEC-1997.
XX
PF 17-JUN-1997; 97EP-0304249.
XX
PR 18-JUN-1996; 96US-0019991.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (UYSF-) UNIV SOUTH FLORIDA.
PA (UNIW) UNIV WASHINGTON.
XX
PI Barton AJL, Goate AM, Hardy J;
XX
DR WPI; 1998-044335/05.
DR P-PSDB; AAW42375.
XX
PT DNA encoding presenelin I - useful for diagnosis of Alzheimer's
PT disease, drug screening, etc.
XX
PS Claim 1; Page 12-13; 20pp; English.
XX
CC This cDNA sequence codes for a 463-amino acid human presenilin I
CC (PS-I) gene product (see AAW42375). A novel variant of PS-1 encoded
CC by a clone isolated from a human cerebellar cDNA library contains a
CC 4-amino acid insertion (VRSQ) between residues 26 and 27. This
CC variant arises from alternative use of a 5' exon donor site in the
CC exon 3/intron 3 boundary of the PS-1 gene. The 4-amino acid motif
CC can be used as a diagnostic marker for variants of presenilin genes
CC associated with Alzheimer's disease and familial adult onset
CC Alzheimer's disease (FAD). Methods are provided for detecting the
CC presence or absence of a 4-amino acid motif (VRXQ, where X is a
CC hydrophilic amino acid) in expressed proteins that arise from
CC aberrant alternative splicing of pre-mRNA in genes associated with
CC normal neurological function, which are useful for detecting
CC neurodegenerative disease. The presence of these variants suggest
CC that mutational events have occurred. Methods to measure the
CC levels of gene expression of such genes to detect neurodegenerative
CC diseases are provided. Nucleotide sequences and intron-exon
CC junctional sequences of examples of this splicing variant and
CC probes (see AAV03247-49) for detecting this variant which are useful
CC as diagnostic reagents are also provided.
XX
SQ Sequence 1750 BP; 442 A; 391 C; 428 G; 478 T; 11 other;

Query Match 16.3%; Score 245; DB 19; Length 1750;
Best Local Similarity 54.5%; Pred. No. 1.8e-46;
Matches 664; Conservative 0; Mismatches 515; Indels 40; Gaps 7;

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Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178

Db        355 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 414

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238

Db        415 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 474

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298

Db        475 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 531

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358

Db        532 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 591

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418

Db        592 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 651

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478

Db        652 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 711

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538

Db        712 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 771

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598

Db        772 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 831

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658

Db        832 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 891

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718

Db        892 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 951

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778

Db        952 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1011

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838

Db       1012 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1058
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Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db       1059 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 1113

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db       1114 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1171

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db       1172 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1231

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db       1232 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1281

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db       1282 CAGAGGAAAGGGGAGTAAAACTTGGATTGCCAGATTTCATTTTCTACAGTGTTCTGGTTG 1341

Qy       1139 GCAAGGCTTCATCGTACTTT------GACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db       1342 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1401

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db       1402 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1461

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db       1462 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1521

Qy       1312 CCCCATTTGTTACACAAGT 1330
Db       1522 AGCCTTTTATGGACCAATT 1540
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```
RESULT 25
AAT85333
ID   AAT85333 standard; DNA; 2765 BP.
XX
AC   AAT85333;
XX
DT   09-DEC-1997  (first entry)
XX
DE   Human mutant S182 gene, PS1 locus, related to Alzheimer's disease.
XX
KW   Mutant; antisense; antibody; vaccine; Alzheimer's disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= Mutant_PS1
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FT                   /*tag=  b
FT                   /note= "The wild-type PS1 has t replacing the
FT                         mutant c at this position"
FT   mutation        1039
FT                   /*tag=  c
FT                   /note= "The wild-type PS1 has c replacing the
FT                         mutant t at this position"
FT   mutation        1054
FT                   /*tag=  d
FT                   /note= "The wild-type PS1 has g replacing the
FT                         mutant a at this position"
XX
PN   WO9708319-A1.
XX
PD   06-MAR-1997.
XX
PF   03-SEP-1996;   96WO-US14114.
XX
PR   30-AUG-1996;   96US-0706344.
PR   31-AUG-1995;   95US-0003054.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Tanzi RE,  Wasco W;
XX
DR   WPI; 1997-179276/16.
DR   P-PSDB; AAW27177.
XX
PT   Chromosome 14 early-onset familial Alzheimer's disease gene PS1
PT   mutants - useful for diagnosing likelihood of developing Alzheimer's
PT   disease, also anti-sense sequences, antibodies and vaccines to delay
PT   onset
XX
PS   Claim 2; Page 74-77; 99pp; English.
XX
CC   The present sequence represents the human mutant S182 gene, PS1 locus.
CC   Mutant PS1 produces a gene product that increases the probability of
CC   Alzheimer's disease. A nucleic acid sequence able to hybridise to
CC   sequences coding for a mutant PS1 polypeptide can be used as probes for
CC   diagnosing an increased likelihood of contracting Alzheimer's disease.
CC   Antibodies against the mutant polypeptide can also be used for this
CC   purpose. Vectors containing or expressing a nucleic acid molecule,
CC   protein or antibody specific for mutant PS1 can be administered to a
CC   patient to reduce the likelihood, or delay the onset, of Alzheimer's
CC   disease, e.g. anti-sense RNA expression can be used to decrease
CC   expression of the PS1 peptide. Transgenic animals expressing the
CC   Alzheimer's disease protein can be used to test candidate therapeutics
CC   and to investigate the normal role of PS1. The PS1 peptide may also be
CC   included in pharmaceutical compositions (vaccines) for Alzheimer's
CC   disease therapy.
XX
SQ   Sequence 2765 BP; 716 A; 625 C; 651 G; 772 T; 1 other;

  Query Match             16.3%;  Score 245;  DB 18;  Length 2765;
  Best Local Similarity   54.5%;  Pred. No. 2e-46;
  Matches  664;  Conservative    0;  Mismatches  515;  Indels   40;  Gaps    7;
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Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db        442 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 501

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
Db        502 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 561

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db        562 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 618

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db        619 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 678

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db        679 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 738

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db        739 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 798

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db        799 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 858

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db        859 ATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 918
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Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db        919 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 978

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db        979 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGCGTC 1038

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db       1039 TGAAAGGTCCACTTCATATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 1098

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db       1099 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 1145

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db       1146 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGCATAATGCAG 1200

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db       1201 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1258

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db       1259 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1318

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db       1319 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGT----------ATCCTCGCTGGTGAAGACC 1368

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db       1369 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATTTCATTTTCTACAGTGTTCTGGTTG 1428

Qy       1139 GCAAGGCTTCATCGTACTTT------GACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db       1429 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1488

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db       1489 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1548

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db       1549 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1608

Qy       1312 CCCCATTTGTTACACAAGT 1330
Db       1609 AGCCTTTTATGGACCAATT 1627
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RESULT 26
AAX90185
ID AAX90185 standard; DNA; 1404 BP.
XX
AC AAX90185;
XX
DT 23-SEP-1999 (first entry)
XX
DE Mouse presenilin-1 encoding DNA.
XX
KW Presenilin-1; mutation; gene mutant animal; Alzheimer's disease; ss.
XX
OS Mus sp.
XX
PN WO9934670-A1.
XX
PD 15-JUL-1999.
XX
PF 07-JAN-1999; 99WO-JP00015.
XX
PR 08-JAN-1998; 98JP-0002191.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
XX
PI Takeda J, Takeda M;
XX
DR WPI; 1999-430307/36.
DR P-PSDB; AAY24420.
XX
PT Mutant presenilin-1 gene-introduced animals, useful as model animals
PT for study of Alzheimer's diseases in human and screening substances
PT for prevention and/or treatment of the diseases
XX
PS Disclosure; Page 56-58; 64pp; Japanese.
XX
CC The present invention describes a gene mutant animal having a non-human
CC mutant presenilin gene. The mutant presenilin gene causes amino acid
CC substitutions at 1 or more positions of 79, 82, 96, 115, 120, 135, 139,
CC 143, 146, 163, 209, 213, 231, 235, 246, 250, 260, 263, 264, 267, 269,
CC 280, 285, 286, 290, 318, 384, 392, 410, 426 and 436, with corresponding
CC N-terminals being e.g. A79V, V82L, A426 and P436S, particularly by
CC replacing isoleucine of position 213 by another amino-acid especially
CC threonine. The gene mutant animals e.g. mice can be used as model
CC animals for the study of human Alzheimer's diseases and to screen and
CC evaluate substances as candidates for prevention and/or therapy of
CC Alzheimer's diseases in patients. They can over-produce amyloid
CC beta protein by the presenilin-1 gene to cause nerve cell death or
CC peeling off in the hippocampus earlier. Such animals are being
CC pathologically close to human patients with Alzheimer's diseases. The
CC present sequence encodes mouse presenilin-1, as given in the present
CC invention.
XX
SQ Sequence 1404 BP; 354 A; 362 C; 343 G; 345 T; 0 other;

Query Match 16.2%; Score 243.2; DB 20; Length 1404;
Best Local Similarity 54.4%; Pred. No. 4.4e-46;
Matches 644; Conservative 0; Mismatches 498; Indels 42; Gaps 6;

```
Qy        116 AAGAAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTC 175
Db        191 AACAAGATGAGGAGGAAGACGAAGAGCTGACATTGAAATATGGAGCCAAGCATGTCATCA 250

Qy        176 ATCTATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTA 235
Db        251 TGCTCTTTGTCCCCGTGACCCTCTGCATGGTCGTCGTCGTGGCCACCATCAAATCAGTCA 310

Qy        236 CGTTTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAG 295
Db        311 GCTTCTATACCCGGAAGGACG---GTCAGCTAATCTACACCCCATTCACAGAAGACACTG 367

Qy        296 ACAGTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGG 355
Db        368 AGACTGTAGGCCAAAGAGCCCTGCACTCGATCCTGAATGCGGCCATCATGATCAGTGTCA 427

Qy        356 TCGTTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTC 415
Db        428 TTGTCATTATGACCATCCTCCTGGTGGTCCTGTATAAATACAGGTGCTACAAGGTCATCC 487

Qy        416 ATGGATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGC 475
Db        488 ACGCCTGGCTTATTATTTCATCTCTGTTGTTGCTGTTCTTTTTTTCGTTCATTTACTTAG 547

Qy        476 AAGAAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGG 535
Db        548 GGGAAGTATTTAAGACCTACAATGTCGCCGTGGACTACGTTACAGTAGCACTCCTAATCT 607

Qy        536 GTAACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAAC 595
Db        608 GGAATTTTGGTGTGGTCGGGATGATTGCCATCCACTGGAAAGGCCCCCTTCGACTGCAGC 667

Qy        596 AGTTCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAG 655
Db        668 AGGCGTATCTCATTATGATCAGTGCCCTCATGGCCCTGGTATTTATCAAGTACCTCCCCG 727
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Qy        656 AATGGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCA 715
              ||||||| |  ||| |  |  ||  ||| || || || |  ||| |||| || ||  |
Db        728 AATGGACCGCATGGCTCATCTTGGCTGTGATTTCAGTATATGATTTGGTGGCTGTTTTAT 787

Qy        716 CACCAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTT 775
              || ||||| ||| |  |     |||| ||||| || ||||| ||||| ||| |  | |
Db        788 GTCCCAAAGGCCCACTTCGTATGCTGGTTGAAACAGCTCAGGAAAGAAATGAGACTCTCT 847

Qy        776 TCCCGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTG 835
              | || || || || ||||| ||   | |  | |     |  ||   | |  ||| ||  |
Db        848 TTCCAGCTCTTATCTATTCCTCAACAATGGTGT---GGTTGGTGAATATGGCTGAAGGAG 904

Qy        836 AAAACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTC 895
              |       |  |     | | ||| | |    |  | |  || ||    | |||
Db        905 ACCCAGAAGCCCAAAGGAGGGTACCCAAGAACCCCAAGTATAACACACAAAGAGCGGAGA 964

Qy        896 CTGGAGAGGCGAGTTGTTCATCT-GAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCT 954
              |       |    ||   ||| | |||    |    | |   |||||   |
Db        965 GAGAGACACAGGACAGTGGTTCTGGGAACGATGATGGTGGCTTCAGTGAGGAGTGGGAGG 1024

Qy        955 CAAAAAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGG 1014
              |  |||| |  | ||   | |      |  ||| ||
Db       1025 CCCAAAGAGACAGTCACCTGGGGCCTCATCGCTCCA---------------------- 1060

Qy       1015 GTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCAC 1074
                |  |||  |  ||||    |      |    |    || | |    ||  |
Db       1061 ----CTCCCGAGTCAAGAGCTGCTGTCCAGGAACTTTCTGGGAGCATTCTAACGAGTGAA 1116

Qy       1075 GAAGAGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTC 1134
              ||   ||| || ||||| || |||||||| ||||| || ||||||||||||  ||||||
Db       1117 GACCCGGAGGAAAGAGGAGTAAAACTTGGACTGGGAGATTTCATTTTCTACAGTGTTCTG 1176

Qy       1135 CTCGGCAAGGCTTCATCGTACT------TTGACTGGAACACGACTATCGCTTGTTATGTG 1188
               | || ||||| ||| |   |         ||||||||||| || || || || | |||
Db       1177 GTTGGTAAGGCCTCAGCAACCGCCAGTGGAGACTGGAACACAACCATAGCCTGCTTTGTA 1236

Qy       1189 GCCATTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTC 1248
              ||||| || ||||| || ||| | ||  |  |||||||||||| | |||||   |||  |
Db       1237 GCCATACTGATCGGCCTGTGCCTTACATTACTCCTGCTCGCCATTTTCAAGAAAGCGTTG 1296

Qy       1249 CCGGCTCT-GCAATTTCCATTTTCTCCGGACTCATTTTTTACTT 1291
              || || ||  | || |||||   || ||| ||| | || |||||
Db       1297 CCAGCCCTCCCCATCTCCATCACCTTCGGGCTCGTGTTCTACTT 1340
```

RESULT 27
AAT40030
ID AAT40030 standard; DNA; 1964 BP.
XX
AC AAT40030;
XX
DT 23-JUL-1997 (first entry)
XX
DE Murine presenilin-1 wild type coding sequence.
XX
KW Presenilin-1; mouse; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW depression; antibody; gene expression modulator; therapy; ss.
XX
OS Mus musculus.
XX
FH Key   Location/Qualifiers
FT CDS   188..1591
FT   /*tag= a
FT   /product= presenilin-1
XX
PN WO9634099-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-CA00263.
XX
PR 31-JUL-1995; 95US-0509359.
PR 28-APR-1995; 95US-0431048.
PR 28-JUN-1995; 95US-0496841.
XX
PA (HSCR-) HSC RES & DEV LP.
PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.
XX
PI Fraser PE, Rommens JM, St George-Hyslop PH;
XX
DR WPI; 1996-497631/49.
DR P-PSDB; AAW05735.
XX
PT New presenilin genes - useful for diagnosis, therapy and drug
PT screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS Claim 8; Page 145-146; 178pp; English.
XX
CC This sequence represents the coding sequence for the murine
CC presenilin-1. AAT40028 and AAT40029 represent the coding sequences for
CC the two different forms of wild type human presenilin-1 (PS-1). The form
CC represented by AAT40029 results from alternate splicing of the genomic
CC DNA sequence. AAT40031 represents the coding sequence for wild type human
CC PS-2. The presenilins are a family of highly conserved integral membrane
CC proteins with a common structural motif, common alternate splicing
CC patterns, and common mutational hot spot regions. Mutations in PS genes
CC are implicated in familial Alzheimer's disease (AD) and possibly other
CC diseases such as cerebral haemorrhage, schizophrenia, depression etc., so
CC detection of mutations in these sequences can be used for diagnosis of
CC these diseases. The encoded proteins, or vectors that express them or
CC containing antisense sequences, antibodies selective for mutant forms of
CC the encoded proteins (such as AAW05736) and modulators of PS gene
CC expression are potentially useful for treatment of AD etc. Transgenic
CC animals are useful as models for drug screening. The antibodies can also
CC be used e.g. for affinity purification and in immunoassays.
XX
SQ Sequence 1964 BP; 503 A; 503 C; 496 G; 460 T; 2 other;

Query Match 16.2%; Score 243.2; DB 17; Length 1964;
Best Local Similarity 54.4%; Pred. No. 4.8e-46;
Matches 644; Conservative 0; Mismatches 498; Indels 42; Gaps 6;

```
Qy        116 AAGAAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTC 175
              || |||| ||  | |  |  |||||   |    ||||||| |||||    || || ||
Db        378 AACAAGATGAGGAGGAAGACGAAGAGCTGACATTGAAATATGGAGCCAAGCATGTCATCA 437

Qy        176 ATCTATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTA 235
              || ||||| || ||| | || |||||||   | || ||    || || ||  |  | |
Db        438 TGCTCTTTGTCCCCGTGACCCTCTGCATGGTCGTCGTCGTGGCCACCATCAAATCAGTCA 497

Qy        236 CGTTTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAG 295
              || ||||  |  ||  | |   | ||  || | |     || ||       || || |
Db        498 GCTTCTATACCCGGAAGGACG---GTCAGCTAATCTACACCCCATTCACAGAAGACACTG 554

Qy        296 ACAGTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGG 355
              | | | |   | |  |   ||  ||  |    |||||   | |||||  |  | ||
Db        555 AGACTGTAGGCCAAAGAGCCCTGCACTCGATCCTGAATGCGGCCATCATGATCAGTGTCA 614

Qy        356 TCGTTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTC 415
              | ||  | |||||  | || ||| | ||  | ||||||||||| ||  || ||| | || |
Db        615 TTGTCATTATGACCATCCTCCTGGTGGTCCTGTATAAATACAGGTGCTACAAGGTCATCC 674

Qy        416 ATGGATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGC 475
              | |  |||||||||  |     | |  |  | || ||| | ||  |    || ||  |
Db        675 ACGCCTGGCTTATTATTTCATCTCTGTTGTTGCTGTTCTTTTTTTCGTTCATTTACTTAG 734

Qy        476 AAGAAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGG 535
              |||||  | || |  | | ||||  |       |    |    ||      |   | |
Db        735 GGGAAGTATTTAAGACCTACAATGTCGCCGTGGACTACGTTACAGTAGCACTCCTAATCT 794

Qy        536 GTAACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAAC 595
              | || | ||| ||  |||| |||||    || || |||||||| ||  | || |||||  |
Db        795 GGAATTTTGGTGTGGTCGGGATGATTGCCATCCACTGGAAAGGCCCCCTTCGACTGCAGC 854
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Qy        596 AGTTCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAG 655
              ||   || || ||||  ||   ||| || ||||| ||||| |||||||||||||||| || |
Db        855 AGGCGTATCTCATTATGATCAGTGCCCTCATGGCCCTGGTATTTATCAAGTACCTCCCCG 914

Qy        656 AATGGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCA 715
              ||||||| |  ||| |  |  ||  ||| || || || |  ||| |||| || ||  |
Db        915 AATGGACCGCATGGCTCATCTTGGCTGTGATTTCAGTATATGATTTGGTGGCTGTTTTAT 974

Qy        716 CACCAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTT 775
                || ||||| ||| |  |     |||| ||||| || ||||| ||||| ||| |  | |
Db        975 GTCCCAAAGGCCCACTTCGTATGCTGGTTGAAACAGCTCAGGAAAGAAATGAGACTCTCT 1034

Qy        776 TCCCGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTG 835
              | || || || || ||||| ||    | |  | |     |  ||   | |  ||| ||  |
Db       1035 TTCCAGCTCTTATCTATTCCTCAACAATGGTGT---GGTTGGTGAATATGGCTGAAGGAG 1091

Qy        836 AAAACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTC 895
              |       |  |     | | ||| | |    |  | |  || ||    | |||
Db       1092 ACCCAGAAGCCCAAAGGAGGGTACCCAAGAACCCCAAGTATAACACACAAAGAGCGGAGA 1151

Qy        896 CTGGAGAGGCGAGTTGTTCATCT-GAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCT 954
                |       |    ||  ||| | ||||   |    | |  |||||  |
Db       1152 GAGAGACACAGGACAGTGGTTCTGGGAACGATGATGGTGGCTTCAGTGAGGAGTGGGAGG 1211

Qy        955 CAAAAAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGG 1014
              |  |||| |  | ||   | |      |  ||| ||
Db       1212 CCCAAAGAGACAGTCACCTGGGGCCTCATCGCTCCA---------------------- 1247

Qy       1015 GTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCAC 1074
                |  |||  |  ||||     |      |    |    || | |    ||  |
Db       1248 ----CTCCCGAGTCAAGAGCTGCTGTCCAGGAACTTTCTGGGAGCATTCTAACGAGTGAA 1303

Qy       1075 GAAGAGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTC 1134
              ||   ||| || ||||| || |||||||| |||||  || ||||||||||||  ||||||
Db       1304 GACCCGGAGGAAAGAGGAGTAAAACTTGGACTGGGAGATTTCATTTTCTACAGTGTTCTG 1363

Qy       1135 CTCGGCAAGGCTTCATCGTACT------TTGACTGGAACACGACTATCGCTTGTTATGTG 1188
              | || ||||| ||| |   |         |||||||||| || || || || | |||
Db       1364 GTTGGTAAGGCCTCAGCAACCGCCAGTGGAGACTGGAACACAACCATAGCCTGCTTTGTA 1423

Qy       1189 GCCATTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTC 1248
              ||||| || ||||| || ||| | ||  |  ||||||||||| | |||||   |||  |
Db       1424 GCCATACTGATCGGCCTGTGCCTTACATTACTCCTGCTCGCCATTTTCAAGAAAGCGTTG 1483

Qy       1249 CCGGCTCT-GCAATTTCCATTTTCTCCGGACTCATTTTTTACTT 1291
              || || ||  | || |||||   || ||| ||| | || |||||
Db       1484 CCAGCCCTCCCCATCTCCATCACCTTCGGGCTCGTGTTCTACTT 1527


RESULT 28
AAV04668
ID   AAV04668 standard; cDNA; 1964 BP.
XX
AC   AAV04668;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Mouse presenilin-1 cDNA.
XX
KW   Presenilin-1; PS1 gene; mouse; familial Alzheimer's disease; FAD;
KW   cerebral haemorrhage; schizophrenia; depression; epilepsy;
KW   mental retardation; diagnosis; therapy; transgenic animal; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             188..1561
FT                   /*tag=  a
XX
PN   WO9801549-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;    97WO-CA00475.
XX
PR   02-JAN-1997;    97US-0034590.
PR   05-JUL-1996;    96US-0021673.
PR   12-JUL-1996;    96US-0021700.
PR   08-NOV-1996;    96US-0029895.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1998-286355/25.
DR   P-PSDB; AAW23966.
XX
PT   New isolated mutant presenilin-1 genes - useful for developing
PT   products for use in detection, diagnosis and therapy of Alzheimer's
PT   disease and for drug screening
XX
PS   Disclosure; Page 197-199; 238pp; English.
XX
CC   This cDNA clone for a murine presenilin-1 (PS1) homologue (see
CC   AAW23966).  It was isolated from a mouse cDNA library using a DNA
CC   probe from the human PS1 gene (see AAV04666).  Mutations in the
CC   human PS1 and PS2 genes (see AAV04666-68) have been linked to the
CC   development in humans of forms of familial Alzheimer's disease
CC   (FAD).  All amino acids that are mutated in analysed FAD
CC   pedigrees were conserved in the murine homologue.  Use of the
CC   nucleic acids and proteins comprising or derived from presenilins
CC   can be made in screening and diagnosing FAD, identifying and
CC   developing therapeutics for treatment of FAD, and in producing cell
CC   lines and transgenic animals useful as models of FAD.
XX
SQ   Sequence 1964 BP; 503 A; 503 C; 496 G; 460 T; 2 other;

  Query Match           16.2%;  Score 243.2;  DB 19;  Length 1964;
  Best Local Similarity  54.4%;  Pred. No. 4.8e-46;
  Matches  644;  Conservative    0;  Mismatches  498;  Indels   42;  Gaps    6;

Qy        116 AAGAAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTC 175
              || |||| ||  | |  |  |||||   |    ||||||| |||||    || || ||
Db        378 AACAAGATGAGGAGGAAGACGAAGAGCTGACATTGAAATATGGAGCCAAGCATGTCATCA 437

Qy        176 ATCTATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTA 235
                || ||||| || ||| | || |||||||   | || ||    || || ||  |  | |
Db        438 TGCTCTTTGTCCCCGTGACCCTCTGCATGGTCGTCGTCGTGGCCACCATCAAATCAGTCA 497

Qy        236 CGTTTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAG 295
                || ||||  |  ||  | |   | ||  || | |     || ||       || || |
Db        498 GCTTCTATACCCGGAAGGACG---GTCAGCTAATCTACACCCCATTCACAGAAGACACTG 554

Qy        296 ACAGTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGG 355
              | | | | |   | | |   ||   ||  |    |||||   | ||||| |  | ||
Db        555 AGACTGTAGGCCAAAGAGCCCTGCACTCGATCCTGAATGCGGCCATCATGATCAGTGTCA 614

Qy        356 TCGTTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTC 415
              | ||  | |||||  | || ||| | ||  | ||||||||||  ||  || ||| | || |
Db        615 TTGTCATTATGACCATCCTCCTGGTGGTCCTGTATAAATACAGGTGCTACAAGGTCATCC 674

Qy        416 ATGGATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGC 475
              | |  |||||||||  |       | |  |  | || ||| | ||  |    || ||  |
Db        675 ACGCCTGGCTTATTATTTCATCTCTGTTGTTGCTGTTCTTTTTTTCGTTCATTTACTTAG 734

Qy        476 AAGAAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGG 535
                |||||  | ||  |  | | ||||  |       |    |    ||     |  | |
Db        735 GGGAAGTATTTAAGACCTACAATGTCGCCGTGGACTACGTTACAGTAGCACTCCTAATCT 794

Qy        536 GTAACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAAC 595
              | || | ||| ||  |||| |||||    || || |||||||| ||  | || ||||| |
Db        795 GGAATTTTGGTGTGGTCGGGATGATTGCCATCCACTGGAAAGGCCCCCTTCGACTGCAGC 854

Qy        596 AGTTCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAG 655
              ||   || || ||||  ||   ||| || ||||| ||||| |||||||||||||||| || |
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Db        855 AGGCGTATCTCATTATGATCAGTGCCCTCATGGCCCTGGTATTTATCAAGTACCTCCCCG 914

Qy        656 AATGGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCA 715
              ||||||| |  ||| |  |  ||  ||| || || || |  ||| |||| || ||  |
Db        915 AATGGACCGCATGGCTCATCTTGGCTGTGATTTCAGTATATGATTTGGTGGCTGTTTTAT 974

Qy        716 CACCAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTT 775
                || ||||| ||| |  |     |||| ||||| || ||||| ||||| ||| |  | |
Db        975 GTCCCAAAGGCCCACTTCGTATGCTGGTTGAAACAGCTCAGGAAAGAAATGAGACTCTCT 1034

Qy        776 TCCCGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTG 835
              | || || || || ||||| ||   | |  | |     |  ||   | |  ||| ||  |
Db       1035 TTCCAGCTGTTATCTATTCCTCAACAATGGTGT---GGTTGGTGAATATGGCTGAAGGAG 1091

Qy        836 AAAACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTC 895
              |         |  |     | | ||| | |     |  | |  || ||    | |||
Db       1092 ACCCAGAAGCCCAAAGGAGGGTACCCAAGAACCCCAAGTATAACACACAAAGAGCGGAGA 1151

Qy        896 CTGGAGAGGCGAGTTGTTCATCT-GAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCT 954
                |       |    ||  ||| | ||||  |    |  |   |||||   |
Db       1152 GAGAGACACAGGACAGTGGTTCTGGGAACGATGATGGTGGCTTCAGTGAGGAGTGGGAGG 1211

Qy        955 CAAAAAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGG 1014
              |  |||| |  | ||   | |      |  ||| ||
Db       1212 CCCAAAGAGACAGTCACCTGGGGCCTCATCGCTCCA---------------------- 1247

Qy        1015 GTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCAC 1074
               |  |||  |   ||||     |      |    || | |    ||  |
Db        1248 ----CTCCCGAGTCAAGAGCTGCTGTCCAGGAACTTTCTGGGAGCATTCTAACGAGTGAA 1303

Qy        1075 GAAGAGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTC 1134
               ||   ||| || ||||| || |||||||| ||||| || ||||||||||  ||||||
Db        1304 GACCCGGAGGAAAGAGGAGTAAAACTTGGACTGGGAGATTTCATTTTCTACAGTGTTCTG 1363

Qy        1135 CTCGGCAAGGCTTCATCGTACT------TTGACTGGAACACGACTATCGCTTGTTATGTG 1188
               | || ||||| ||| |   |          |||||||||||| || || || || | |||
Db        1364 GTTGGTAAGGCCTCAGCAACCGCCAGTGGAGACTGGAACACAACCATAGCCTGCTTTGTA 1423

Qy        1189 GCCATTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTC 1248
               ||||| || ||||| || ||| | ||  |  |||||||||||| | |||||   ||| |
Db        1424 GCCATACTGATCGGCCTGTGCCTTACATTACTCCTGCTCGCCATTTTCAAGAAAGCGTTG 1483

Qy        1249 CCGGCTCT-GCAATTTCCATTTTCTCCGGACTCATTTTTTACTT 1291
               || || ||  | || |||||   || ||| ||| | || |||||
Db        1484 CCAGCCCTCCCCATCTCCATCACCTTCGGGCTCGTGTTCTACTT 1527
```

RESULT 29
AAT64819
ID AAT64819 standard; cDNA; 2681 BP.
XX
AC AAT64819;
XX
DT 25-MAR-1998 (first entry)
XX
DE Tumour suppressor inhibited pathway gene TSIP2.
XX
KW Tumour suppressor activated pathway; tumour suppressor inhibited pathway;
KW TSAP; TSIP; HUMSIAH; Human Homologue of the Drosophila seven in absentia;
KW apoptosis; p53; cancer; Alzheimer's disease; probe; amplification; PCR;
KW primer; hybridisation; diagnosis; ss.
XX
OS Mus sp.
XX
PN WO9722695-A2.
XX
PD 26-JUN-1997.
XX
PF 20-DEC-1996; 96WO-FR02061.
XX
PR 18-APR-1996; 96FR-0004853.
PR 20-DEC-1995; 95FR-0015146.
XX
PA (DAUS-) FOND DAUSSET-CEPH JEAN.
XX
PI Amson R, Cohen D, Talerman A;
XX
DR WPI; 1997-341686/31.
XX
PT New genes activated or inhibited during apoptosis - useful for
PT treatment of, and for assessing risk of developing, cancer and
PT Alzheimer's disease
XX
PS Claim 1; Fig 8; 51pp; French.
XX
CC This is the nucleotide sequence of the tumour suppressor inhibited
CC pathway gene 2 (TSIP2). The sequences AAT64813-T64823 represent genes
CC of the tumour suppressor activated pathway (TSAP 1-8, also human TSAP 3,
CC also designated HUMSIAH, i.e. Human Homologue of the Drosophila seven
CC in absentia gene) or of the tumour suppressor inhibited pathway (TSIP 1
CC and 2). Expression of TSAP genes is induced during apoptosis while that
CC of TSIP is induced by tumour suppressors and inhibited during apoptosis,
CC especially where apoptosis is induced by p53. The sequences, vectors
CC containing them or compounds that induce their expression are useful for
CC treatment of cancer and Alzheimer's disease. Fragments of the sequences
CC are useful as probes and amplification primers to determine
CC predisposition to these diseases by detecting abnormalities in the
CC genes.
XX
SQ Sequence 2681 BP; 663 A; 709 C; 658 G; 650 T; 1 other;

Query Match 16.2%; Score 243.2; DB 18; Length 2681;
Best Local Similarity 54.4%; Pred. No. 5.3e-46;
Matches 644; Conservative 0; Mismatches 498; Indels 42; Gaps 6;

```
Qy         116 AAGAAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTC 175
               || |||| ||  | |  |  |||||   |    ||||||| |||||    || || ||
Db         445 AACAAGATGAGGAGGAAGACGAAGAGCTGACATTGAAATATGGAGCCAAGCATGTCATCA 504

Qy         176 ATCTATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTA 235
                 || ||||| || ||| | || |||||||   | || ||    || || ||  |  | |
Db         505 TGCTCTTTGTCCCCGTGACCCTCTGCATGGTCGTCGTCGTGGCCACCATCAAATCAGTCA 564

Qy         236 CGTTTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAG 295
                 || ||||  |  ||  | |   | ||  || | |     || ||       || || |
Db         565 GCTTCTATACCCGGAAGGACG---GTCAGCTAATCTACACCCCATTCACAGAAGACACTG 621

Qy         296 ACAGTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGG 355
               | | | | |   | |  |   ||   ||  |    |||||   | |||||  |  | ||
Db         622 AGACTGTAGGCCAAAGAGCCCTGCACTCGATCCTGAATGCGGCCATCATGATCAGTGTCA 681

Qy         356 TCGTTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTC 415
               | ||  | |||||  | || ||| | ||  | ||||||||||| ||  || ||| | || |
Db         682 TTGTCATTATGACCATCCTCCTGGTGGTCCTGTATAAATACAGGTGCTACAAGGTCATCC 741

Qy         416 ATGGATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGC 475
               | |  |||||||||| |      | |  |  | || ||| | ||   |    || ||  |
Db         742 ACGCCTGGCTTATTATTTCATCTCTGTTGTTGCTGTTCTTTTTTTCGTTCATTTACTTAG 801

Qy         476 AAGAAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGG 535
                 |||||  | || |  | | ||||  |       |    |    ||      |   | |
Db         802 GGGAAGTATTTAAGACCTACAATGTCGCCGTGGACTACGTTACAGTAGCACTCCTAATCT 861

Qy         536 GTAACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAAC 595
               | || | ||| ||  |||| |||||     || || |||||||| ||  | || ||||| |
Db         862 GGAATTTTGGTGTGGTCGGGATGATTGCCATCCACTGGAAAGGCCCCCTTCGACTGCAGC 921

Qy         596 AGTTCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAG 655
               ||   || || |||| ||  ||| || ||||| ||||| ||||||||||||||| || |
Db         922 AGGCGTATCTCATTATGATCAGTGCCCTCATGGCCCTGGTATTTATCAAGTACCTCCCCG 981

Qy         656 AATGGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCA 715
               |||||||  |  ||| |  |  ||  ||| || || || |  ||| |||| || ||  |
Db         982 AATGGACCGCATGGCTCATCTTGGCTGTGATTTCAGTATATGATTTGGTGGCTGTTTTAT 1041

Qy         716 CACCAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTT 775
```

```
Db       1042 GTCCCAAAGGCCCACTTCGTATGCTGGTTGAAACAGCTCAGGAAAGAAATGAGACTCTCT 1101

Qy        776 TCCCGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTG 835

Db       1102 TTCCAGCTCTTATCTATTCCTCAACAATGGTGT---GGTTGGTGAATATGGCTGAAGGAG 1158

Qy        836 AAAACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTC 895

Db       1159 ACCCAGAAGCCCAAAGGAGGGTACCCAAGAACCCCAAGTATAACACACAAAGAGCGGAGA 1218

Qy        896 CTGGAGAGGCGAGTTGTTCATCT-GAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCT 954

Db       1219 GAGAGACACAGGACAGTGGTTCTGGGAACGATGATGGTGGCTTCAGTGAGGAGTGGGAGG 1278

Qy        955 CAAAAAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGG 1014

Db       1279 CCCAAAGAGACAGTCACCTGGGGCCTCATCGCTCCA---------------------- 1314

Qy       1015 GTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCAC 1074

Db       1315 ----CTCCCGAGTCAAGAGCTGCTGTCCAGGAACTTTCTGGGAGCATTCTAACGAGTGAA 1370

Qy       1075 GAAGAGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTC 1134

Db       1371 GACCCGGAGGAAAGAGGAGTAAAACTTGGACTGGGAGATTTCATTTTCTACAGTGTTCTG 1430

Qy       1135 CTCGGCAAGGCTTCATCGTACT------TTGACTGGAACACGACTATCGCTTGTTATGTG 1188

Db       1431 GTTGGTAAGGCCTCAGCAACCGCCAGTGGAGACTGGAACACAACCATAGCCTGCTTTGTA 1490

Qy       1189 GCCATTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTC 1248

Db       1491 GCCATACTGATCGGCCTGTGCCTTACATTACTCCTGCTCGCCATTTTCAAGAAAGCGTTG 1550

Qy       1249 CCGGCTCT-GCAATTTCCATTTTCTCCGGACTCATTTTTTACTT 1291

Db       1551 CCAGCCCTCCCCATCTCCATCACCTTCGGGCTCGTGTTCTACTT 1594
```

```
RESULT 30
AAT40043
ID   AAT40043 standard; DNA; 1895 BP.
XX
AC   AAT40043;
XX
DT   25-JUL-1997  (first entry)
XX
DE   Presenilin homologue.
XX
KW   Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW   familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW   depression; antibody; gene expression modulator; therapy; ss.
XX
OS   Drosophila melanogaster.
XX
FH   Key             Location/Qualifiers
FT   CDS             140..1765
FT                   /*tag= a
FT                   /product= presenilin
XX
PN   WO9634099-A2.
XX
PD   31-OCT-1996.
XX
PF   29-APR-1996;    96WO-CA00263.
XX
PR   31-JUL-1995;    95US-0509359.
PR   28-APR-1995;    95US-0431048.
PR   28-JUN-1995;    95US-0496841.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1996-497631/49.
DR   P-PSDB; AAW05767.
XX
PT   New presenilin genes - useful for diagnosis, therapy and drug
PT   screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS   Claim 33; Page 152-154; 178pp; English.
XX
CC   This sequence represents a homologue of human presenilin, isolated from
CC   Drosophila melanogaster. AAT40028 and AAT40029 represent the coding
CC   sequences for the two different forms of wild type human presenilin-1
CC   (PS-1). The form represented by AAT40029 results from alternate splicing
CC   of the genomic DNA sequence. AAT40031 represents the coding sequence for
CC   wild type human PS-2. The presenilins are a family of highly conserved
CC   integral membrane proteins with a common structural motif, common
CC   alternate splicing patterns, and common mutational hot spot regions.
CC   Mutations in PS genes are implicated in familial Alzheimer's disease (AD)
CC   and possibly other diseases such as cerebral haemorrhage, schizophrenia,
CC   depression etc., so detection of mutations in these sequences can be used
CC   for diagnosis of these diseases. The encoded proteins, or vectors that
CC   express them or containing antisense sequences, antibodies selective for
CC   mutant forms of the encoded proteins (such as AAW05736) and modulators of
CC   PS gene expression are potentially useful for treatment of AD etc.
CC   Transgenic animals are useful as models for drug screening. The
CC   antibodies can also be used e.g. for affinity purification and in
CC   immunoassays.
XX
SQ   Sequence 1895 BP; 456 A; 500 C; 468 G; 471 T; 0 other;
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  Query Match           15.1%;  Score 226.2;  DB 17;  Length 1895;
  Best Local Similarity  59.4%;  Pred. No. 3.8e-42;
  Matches  403;  Conservative    0;  Mismatches  273;  Indels    3;  Gaps    1;

Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190

Db        411 TGGAGGAAGAGCAGGGCCTGAAATACGGGGCCCAGCATGTGATCAAGTTATTCGTCCCCG 470

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250

Db        471 TCTCCCTTTGCATGCTGGTAGTGGTGGCTACCATCAACTCCATCAGCTTCTACA---ACA 527

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310

Db        528 GCACGGATGTCTATCTCCTCTACACACCTTTCCATGAACAATCGCCCGAGCCTAGTGTTA 587

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370

Db        588 AGTTCTGGAGTGCCTTGGCGAACTCCCTGATCCTGATGAGCGTGGTGGTGGTGATGACCT 647

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430

Db        648 TTTTGCTGATTGTTTTGTACAAGAAGCGTTGCTATCGCATCATTCACGGCTGGCTGATTC 707

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490

Db        708 TCTCCTCCTTCATGTTGTTGTTCATTTTTACGTACTTATATTTGGAAGAGCTTCTTCGCG 767

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550

Db        768 CCTATAACATACCGATGGACTACCCTACTGCACTACTGATTATGTGGAACTTTGGAGTGG 827

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610

Db        828 TCGGAATGATGTCCATCCATTGGCAGGGACCTCTGCGGTTGCAGCAAGGATATCTCATTT 887

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670

Db        888 TCGTGGCAGCCTTGATGGCCTTGGTGTTCATTAAATACCTGCCTGAATGGACTGCCTGGG 947

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
```

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Db        948 CTGTATTGGCTGCCATTTCTATTTGGGATCTTATTGCTGTCCTTTCGCCAAGAGGACCCC 1007

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790

Db       1008 TCCGCATTCTGGTGGAAACGGCTCAGGAGCGAAATGAGCAAATCTTCCCCGCTCTGATTT 1067

Qy        791 ATTCGTCTGGAGTCATCTA 809

Db       1068 ATTCATCCACTGTCGTTTA 1086


RESULT 31
ABL29237
ID   ABL29237 standard; DNA; 2048 BP.
XX
AC   ABL29237;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 39184.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 39184; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072)..
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2048 BP; 490 A; 531 C; 500 G; 527 T; 0 other;

  Query Match           15.1%;  Score 226.2;  DB 23;  Length 2048;
  Best Local Similarity   59.4%;  Pred. No. 3.9e-42;
  Matches  403;  Conservative    0;  Mismatches  273;  Indels    3;  Gaps    1;

Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190

Db        587 TGGAGGAAGAGCAGGGCCTGAAATACGGGGCCCAGCATGTGATCAAGTTATTCGTCCCCG 646

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250

Db        647 TCTCCCTTTGCATGCTGGTAGTGGTGGCTACCATCAACTCCATCAGCTTCTACA---ACA 703

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310

Db        704 GCACGGATGTCTATCTCCTCTACACACCTTTCCATGAACAATCGCCCGAGCCTAGTGTTA 763

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370

Db        764 AGTTCTGGAGTGCCTTGGCGAACTCCCTGATCCTGATGAGCGTGGTGGTGGTGATGACCT 823

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430

Db        824 TTTTGCTGATTGTTTTGTACAAGAAGCGTTGCTATCGCATCATTCACGGCTGGCTGATTC 883

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490

Db        884 TCTCCTCCTTCATGTTGTTGTTCATTTTTACGTACTTATATTTGGAAGAGCTTCTTCGCG 943

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550

Db        944 CCTATAACATACCGATGGACTACCCTACTGCACTACTGATTATGTGGAACTTTGGAGTGG 1003

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610

Db       1004 TCGGAATGATGTCCATCCATTGGCAGGGACCTCTGCGGTTGCAGCAAGGATATCTCATTT 1063

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670

Db       1064 TCGTGGCAGCCTTGATGGCCTTGGTGTTCATTAAATACCTGCCTGAATGGACTGCCTGGG 1123

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730

Db       1124 CTGTATTGGCTGCCATTTCTATTTGGGATCTTATTGCTGTCCTTTCGCCAAGAGGACCCC 1183

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790

Db       1184 TCCGCATTCTGGTGGAAACGGCTCAGGAGCGAAATGAGCAAATCTTCCCCGCTCTGATTT 1243

Qy        791 ATTCGTCTGGAGTCATCTA 809

Db       1244 ATTCATCCACTGTCGTTTA 1262


RESULT 32
AAD27444
ID   AAD27444 standard; cDNA; 1404 BP.
XX
AC   AAD27444;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human mutant presenilin 1 (PS1) cDNA #2.
XX
KW   Human; presenilin 1; PS1; amyloid precursor protein; APP; drug screening;
KW   Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
KW   Huntington's disease; amylotrophic lateral sclerosis; Picks disease;
KW   head injury disease; frontal lobe dementia; cerebellar degeneration;
KW   ischaemic injury; schizophrenia; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1400
FT                   /*tag=  a
FT                   /product= "Human mutant presenilin-1 protein"
FT                   /transl_except= (pos:619..626, aa:Val-Val-Gly-Met)
FT                   /note= "There is an apparent deletion of 4 bases
FT                   which alters the reading frame"
FT                   /transl_except= (pos:1152..1154, aa:Xaa)
FT                   /transl_except= (pos:1155..1157, aa:Xaa)
FT                   /note= "Xaa corresponds to unknown amino acid"
XX
PN   WO200202601-A2.
```

XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US16508.
XX
PR 30-JUN-2000; 2000US-215345P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Carter DB, Tomasselli AG;
XX
DR WPI; 2002-140082/18.
DR P-PSDB; AAE17046.
XX
PT Novel isolated mutant presenilin 1 and presenilin 2 polypeptides,
PT useful for screening of drugs for treating pathologies associated with
PT aberrant amyloid precursor protein processing, such as Alzheimer's
PT disease -
XX
PS Claim 52; Page 66; 80pp; English.
XX
CC The invention relates to mutant presenilin 1 (PS1) and presenilin 2
CC (PS2) polypeptides. Presenilin are involved in the processing of amyloid
CC precursor protein (APP) from which major amylodogenic peptides are
CC cleaved. Mutant presenilins are useful for identifying agents that
CC modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
CC presenilin is also useful as a target for screening drugs useful in the
CC treatment of pathologies associated with aberrant amyloid precursor
CC protein processing, such as Alzheimer's disease, Parkinson's disease,
CC multiple sclerosis, Huntington's disease, amylotrophic lateral sclerosis,
CC head injury disease, Picks disease, frontal lobe dementia, cerebellar
CC degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
CC non-human animal is useful for analysing the interaction between APP and
CC mutant presenilin-processing protease in vivo, and for screening anti-
CC Alzheimer's disease drugs in vivo. A transgenic non-human
CC animal is useful for analysing the interaction between APP and mutant
CC presenilin-processing protease in vivo, and for screening anti-
CC Alzheimer's disease drugs in vivo. The present sequence is human
CC mutant PS1 cDNA.
XX
SQ Sequence 1404 BP; 360 A; 312 C; 336 G; 390 T; 6 other;

Query Match 15.1%; Score 225.8; DB 24; Length 1404;
Best Local Similarity 53.9%; Pred. No. 4.3e-42;
Matches 657; Conservative 0; Mismatches 518; Indels 44; Gaps 8;

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Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||   |    ||||||| || ||    || || ||    |
Db        194 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 253

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | ||||| || ||| | || |||||||   |||| ||   ||| ||.||  |  | |  |
Db        254 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 313

Qy        239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
              ||||||  |  ||  |||   ||||  || | |     || ||       || || || |
Db        314 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 370

Qy        299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
              | | |   |||  |   ||   ||| ||   ||||||  | |||||  |  | ||  | |
Db        371 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 430

Qy        359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
              || | |||||  | || ||| | ||| | ||||||||| ||  ||||||  | || ||||
Db        431 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 490

Qy        419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
                |||||||| |      | |  |  | || ||| | ||  |    || ||   ||
Db        491 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 550

Qy        479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
              ||||  | ||||  |   | ||  ||     |    |||    |     | | |
Db        551 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 610

Qy        539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
              | | ||| ||    || |||| |  || || ||||||||||||| | || || || |||
Db        611 ATTTTGGTGT----GGTGTGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 666

Qy        599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
                || || |||  ||   ||| || ||||| ||||| |||||||||||||| || ||||
Db        667 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 726

Qy        659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
              |||||| |||| |  |  ||  ||| || || || |  ||| | || || ||  |  |
Db        727 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATTTAGTGGCTGTTTTGTGTC 786

Qy        719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
              | ||||| ||| |  |     |||| ||||| || ||||||||||| ||  |  |||| |
Db        787 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 846

Qy        779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
              | || || ||||| || ||   | |             | | | ||| || | ||  |
Db        847 CAGCTCTCATTTACTCCTCAACAAT----------GGTGTGGTTGGTGAATATGGCA 893

Qy        839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
                | || |     || ||| |       | ||  || || | ||| |   | | | |
Db        894 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 948

Qy        899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
              |   |     |   || | | ||     || | | |||          |  |
Db        949 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1006

Qy        959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
                | |     | | |     ||||       |   | | | || |     |
Db       1007 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1066

Qy       1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
              |   | ||| |     |   ||| | |||                |     | | ||
Db       1067 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1116

Qy       1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
                || || || || || |||||||  |||| ||       ||||||  ||||||  | |
Db       1117 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATNNNNNNTTCTACAGTGTTCTGGTTG 1176

Qy       1139 GCAAGGCTTCATCGTACTTT------GACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
              | || || ||| |             |||||||||| || || || |||| || ||||
Db       1177 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1236

Qy       1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
              |  | || ||| | ||| | ||  |  | || || ||| | ||||  |||| | || |
Db       1237 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1296

Qy       1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
              ||||  |||| |||||  ||  || ||  |||| ||||||  ||    |  |  |
Db       1297 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1356

Qy       1312 CCCCATTTGTTACACAAGT 1330
                || ||| |    ||| |
Db       1357 AGCCTTTTATGGACCAATT 1375
```

RESULT 33
AAT51253
ID AAT51253 standard; cDNA; 2236 BP.
XX
AC AAT51253;
XX
DT 10-NOV-1997 (first entry)
XX
DE Human AD4 protein coding sequence.
XX
KW Autosomal dominant early-onset Alzheimer's Disease; AD4; STM2;
KW neurodegeneration; senile dementia; human chromosome 1;
KW Volga German kindred; VG; ss.
XX
OS Homo sapiens.

```
XX
FH   Key             Location/Qualifiers
FT   CDS             368..1714
FT                   /*tag=  a
FT                   /product= AD4_protein
XX
PN   WO9703192-A2.
XX
PD   30-JAN-1997.
XX
PF   05-JUL-1996;    96WO-US11386.
XX
PR   14-AUG-1995;    95US-0002328.
PR   07-JUL-1995;    95US-0000956.
PR   28-JUL-1995;    95US-0001675.
PR   11-AUG-1995;    95US-0002174.
XX
PA   (DARW-) DARWIN MOLECULAR CORP.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (VAME-) VA MEDICAL CENT.
XX
PI   Bird TD,  Galas DJ,  Levy-Lahad E,  Mulligan J,  Schellenberg GD;
PI   Tanzi RE,  Wasco W;
XX
DR   WPI; 1997-119048/11.
DR   P-PSDB; AAW11321.
XX
PT   New Alzheimer's disease related gene, AD4 - used to develop prods.
PT   for detecting pre-disposition to or for diagnosis, prevention or
PT   treatment of Alzheimer's disease
XX
PS   Claim 2; Fig 1; 83pp; English.
XX
CC   A genetically isolated group of families with autosomal dominant
CC   early-onset Alzheimer's Disease (AD) has been studied and initial
CC   mapping analyses have predicted the AD locus resides on chromosome 1.
CC   The present cDNA sequence corresponds to the wild-type locus (i.e.
CC   the AD4 gene, also known as STM2) and was isolated from a human
CC   chromosome 1 YAC library. The group of families has been designated
CC   the Volga German (VG) kindreds. The entire gene has been amplified
CC   from VG individuals and unaffected individuals (from VG and
CC   unrelated lineages). Sequence analysis has shown that affected
CC   individuals have a nucleotide change at codon 141 resulting in an
CC   amino acid alteration from Asn to Ile. Portions of a mutant AD4,
CC   especially one in which Asn at position 141 has been replaced by
CC   Ile, can be used in a peptide vaccine. Detection of mutant AD4, for
CC   example using antibodies specific for the protein or using nucleic
CC   acid probes specific for the mutant gene, provides a means of
CC   diagnosing Alzheimer's disease.
XX
SQ   Sequence 2236 BP; 488 A; 584 C; 645 G; 519 T; 0 other;

  Query Match           15.1%;  Score 225.8;  DB 18;  Length 2236;
  Best Local Similarity  59.6%;  Pred. No. 4.9e-42;
  Matches  399;  Conservative    0;  Mismatches  267;  Indels    3;  Gaps    1;

Qy       131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
Db       591 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 650

Qy       191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
Db       651 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 710

Qy       251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
Db       711 AGAATGGA---CAGCTCATCTACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGC 767

Qy       311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
Db       768 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 827

Qy       371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
Db       828 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 887

Qy       431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
Db       888 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 947

Qy       491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
Db       948 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 1007

Qy       551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
Db       1008 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 1067

Qy       611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
Db       1068 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 1127

Qy       671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
Db       1128 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1187

Qy       731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
Db       1188 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1247

Qy       791 ATTCGTCTG 799
Db       1248 ACTCATCTG 1256


RESULT 34
AAT87426
ID   AAT87426 standard; DNA; 2276 BP.
XX
AC   AAT87426;
XX
DT   07-DEC-1997  (first entry)
XX
DE   Full AD4/AD3LP sequence.
XX
KW   AD3; AD4/AD3LP; Alzheimer's disease; chromosome; missegregation;
KW   presenilin; inhibitor; AD; trisomy 21; ss.
XX
OS   Homo sapiens.
XX
PN   WO9707213-A2.
XX
PD   27-FEB-1997.
XX
PF   15-AUG-1996;    96WO-US13314.
XX
PR   16-AUG-1995;    95US-0002448.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Li J,  Potter H;
XX
DR   WPI; 1997-165297/15.
DR   P-PSDB; AAW28508.
XX
PT   Identifying genes which cause chromosome missegregation - useful for
PT   identifying causes of and treatments for diseases, e.g. Alzheimer's
PT   disease, cancer and ageing
XX
PS   Claim 28; Fig 28; 77pp; English.
XX
CC   Identifying genes which cause improper chromosome segregation,
CC   screening for inhibitors of chromosome missegregation and processes
CC   caused by genes encoding chromosome missegregation promoters
CC   was exemplified using Alzheimer's disease.  The sequences
CC   given in AAT87401 to AAT87426 can be used in the above methods.
```

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CC   It is not clear from the figure legend, the figure and the
CC   disclosure of the specification which sequence of Fig 1 and Fig 28
CC   is the AD4/AD3LP or the AD3 sequence.
XX
SQ   Sequence 2276 BP; 494 A; 595 C; 662 G; 525 T; 0 other;

  Query Match            15.1%;  Score 225.8;  DB 18;  Length 2276;
  Best Local Similarity  59.6%;  Pred. No. 4.9e-42;
  Matches  399;  Conservative    0;  Mismatches  267;  Indels    3;  Gaps    1;

Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
              | | ||||||   |   || ||||||||||    |||||  ||    || ||||||||  |
Db        634 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 693

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
              |  | ||  ||||||    ||||  ||    ||  ||  ||   |   |    ||  ||  |   | |
Db        694 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 753

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
              | ||||||   ||  |  | |     || ||      ||| |||  |    | |   ||
Db        754 AGAATGGA---CAGCTCATCTACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGC 810

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
                | |  ||  |    ||  | ||| |||||  |  ||||  ||||  | |||||
Db        811 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 870

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
              |  |  || | ||   |||| || |||    |  || ||| | || ||||| ||| | ||
Db        871 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 930

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
              |       |  | || || ||||| |||||    |||||  |    ||||| || || |
Db        931 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 990

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
                | | |||||  |       |   |       | |||  |      |  | |||| -|| |
Db        991 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 1050

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
              | || ||| |||| || || ||||| || ||  ||   ||||| |||  |||||| || |
Db       1051 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 1110

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
                ||   ||| || ||||| || || || ||||||||||| ||||| ||| | | ||||
Db       1111 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 1170

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
              |  | |||   |  ||||| || |  ||||| || || |||||    || ||||| ||
Db       1171 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1230

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
              |||||    |||| |||||||| |||||||||| ||||| || ||||| || ||||| |
Db       1231 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1290

Qy        791 ATTCGTCTG 799
              | || ||||
Db       1291 ACTCATCTG 1299


RESULT 35
AAD27445
ID   AAD27445 standard; cDNA; 1404 BP.
XX
AC   AAD27445;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human mutant presenilin 1 (PS1) cDNA #3.
XX
KW   Human; presenilin 1; PS1; amyloid precursor protein; APP; drug screening;
KW   Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
KW   Huntington's disease; amylotrophic lateral sclerosis; Picks disease;
KW   head injury disease; frontal lobe dementia; cerebellar degeneration;
KW   ischaemic injury; schizophrenia; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1400
FT                   /*tag= a
FT                   /product= "Human mutant presenilin-1 protein"
FT                   /transl_except= (pos:619..626, aa:Val-Val-Gly-Met)
FT                   /note= "There is an apparent deletion of 4 bases
FT                   which alters the reading frame"
FT                   /transl_except= (pos:768..770, aa:Xaa)
FT                   /transl_except= (pos:771..773, aa:Xaa)
FT                   /transl_except= (pos:1152..1154, aa:Xaa)
FT                   /transl_except= (pos:1155..1157, aa:Xaa)
FT                   /note= "Xaa corresponds to unknown amino acid"
XX
PN   WO200202601-A2.
XX
PD   10-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US16508.
XX
PR   30-JUN-2000; 2000US-215345P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Carter DB,  Tomasselli AG;
XX
DR   WPI; 2002-140082/18.
DR   P-PSDB; AAE17047.
XX
PT   Novel isolated mutant presenilin 1 and presenilin 2 polypeptides,
PT   useful for screening of drugs for treating pathologies associated with
PT   aberrant amyloid precursor protein processing, such as Alzheimer's
PT   disease -
XX
PS   Claim 60; Page 66-67; 80pp; English.
XX
CC   The invention relates to mutant presenilin 1 (PS1) and presenilin 2
CC   (PS2) polypeptides. Presenilin are involved in the processing of amyloid
CC   precursor protein (APP) from which major amylodogenic peptides are
CC   cleaved. Mutant presenilins are useful for identifying agents that
CC   modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
CC   presenilin is also useful as a target for screening drugs useful in the
CC   treatment of pathologies associated with aberrant amyloid precursor
CC   protein processing, such as Alzheimer's disease, Parkinson's disease,
CC   multiple sclerosis, Huntington's disease, amylotrophic lateral sclerosis,
CC   head injury disease, Picks disease, frontal lobe dementia, cerebellar
CC   degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
CC   non-human animal is useful for analysing the interaction between APP and
CC   mutant presenilin-processing protease in vivo, and for screening anti-
CC   Alzheimer's disease drugs in vivo. A transgenic non-human
CC   animal is useful for analysing the interaction between APP and mutant
CC   presenilin-processing protease in vivo, and for screening anti-
CC   Alzheimer's disease drugs in vivo. The present sequence is human
CC   mutant PS1 cDNA.
XX
SQ   Sequence 1404 BP; 359 A; 312 C; 334 G; 387 T; 12 other;

  Query Match            15.0%;  Score 224.6;  DB 24;  Length 1404;
  Best Local Similarity  53.7%;  Pred. No. 8.1e-42;
  Matches  654;  Conservative    0;  Mismatches  521;  Indels   44;  Gaps    8;

Qy        119 AAGACGAAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
              |||| ||  | |  |  || ||   |    |||||||| || ||    || || ||    |
Db        194 AAGATGAGGAAGAAGATGAGGAGCTGACATTGAAATATGGCGCCAAGCATGTGATCATGC 253

Qy        179 TATTTGTGCCGGTGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGT 238
              | ||||| || ||| | || |||||||   |||| ||   ||| || ||  |  | |  |
Db        254 TCTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTCAGCT 313
```

```
Qy      239 TTTATAGTCAAAACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACA 298
Db      314 TTTATACCCGGAAGGATG---GGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGA 370

Qy      299 GTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
Db      371 CTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTG 430

Qy      359 TTCTGATGACAGTTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG 418
Db      431 TTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTCATCCATG 490

Qy      419 GATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAG 478
Db      491 CCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGG 550

Qy      479 AAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTA 538
Db      551 AAGTGTTTAAAACCTATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGA 610

Qy      539 ACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGT 598
Db      611 ATTTTGGTGT----GGTGTGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGG 666

Qy      599 TCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAAT 658
Db      667 CATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAAT 726

Qy      659 GGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACAC 718
Db      727 GGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGATNNNNNNGCTGTTTTGTGTC 786

Qy      719 CAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCC 778
Db      787 CGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTC 846

Qy      779 CGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACGTTCTTGTTACTGCAGTTGAAA 838
Db      847 CAGCTCTCATTTACTCCTCAACAAT------------GGTGTGGTTGGTGAATATGGCA 893

Qy      839 ACACGACAGACCCCCGTGAACCGACGTCGTCAGACTCAAATACTTCTACAGCTTTTCCTG 898
Db      894 GAAGGAGA-----CCCGGAAGCTCAAAGGAGAGTATCCAAAAATTCCAAGTATAATGCAG 948

Qy      899 GAGAGGCGAGTTGTTCATCTGAAACGCCAAAACGGCCAAAAGTGAAACGAATTCCTCAAA 958
Db      949 AAAGCACAGAAAGGGAGTC--ACAAGACACTGTTGCAGAGAATGATGATGGCGGGTTCAG 1006

Qy      959 AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGGTGG 1018
Db     1007 TGAGGAATGGGAAGCCCAGAGGGACAGTCATCTAGGGCCTCATCGCTCTACACCTGAGTC 1066

Qy     1019 AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCCAATTTTCACAGGCACGAAG 1078
Db     1067 ACGAGCTGCTGTCCAGGAACTTTCCAGCAGTAT----------CCTCGCTGGTGAAGACC 1116

Qy     1079 AGGAAGAGAGAGGTGTGAAACTTGGTCTGGGCGACTTCATTTTCTACTCTGTTCTCCTCG 1138
Db     1117 CAGAGGAAAGGGGAGTAAAACTTGGATTGGGAGATNNNNNNTTCTACAGTGTTCTGGTTG 1176

Qy     1139 GCAAGGCTTCATCGTACTTT------GACTGGAACACGACTATCGCTTGTTATGTGGCCA 1192
Db     1177 GTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGCCA 1236

Qy     1193 TTCTTATCGGTCTCTGCTTCACTCTTGTCCTGCTCGCCGTCTTCAAACGAGCACTCCCGG 1252
Db     1237 TATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAG 1296

Qy     1253 CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTTACTTTTGTACCCGCTGGATCATCA 1311
Db     1297 CTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTAC 1356

Qy     1312 CCCCATTTGTTACACAAGT 1330
Db     1357 AGCCTTTTATGGACCAATT 1375
```

RESULT 36
AAD10304
ID AAD10304 standard; DNA; 1346 BP.
XX
AC AAD10304;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human presenilin (PS2) DNA.
XX
KW Human; Par-4; presenilin; PS2; neuroprotective; nuclear factor kappa B;
KW NF-kappa B; neuronal degeneration; spinal muscular atrophy; paralysis;
KW peripheral neuropathy; motorneuron disorder; neurodegenerative disorder;
KW Parkinson's disease; Meniere's disease; multiple sclerosis; Bell's palsy;
KW Huntington's chorea; Down's syndrome; amyotrophic lateral sclerosis; ALS;
KW nerve deafness; Alzheimer's disease; epilepsy; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..1346
FT   /*tag= a
FT   /product= "Human presenilin PS2 protein"
FT   /transl_except= (pos:1051..1052, aa:Glu)
XX
PN WO200151671-A2.
XX
PD 19-JUL-2001.
XX
PF 08-JAN-2001; 2001WO-US00526.
XX
PR 10-JAN-2000; 2000US-0175200.
PR 04-JAN-2001; 2001US-0754949.
XX
PA (SCIO-) SCIOS INC.
XX
PI Mccarthy J, Cordell B;
XX
DR WPI; 2001-451872/48.
DR P-PSDB; AAE05467.
XX
PT Identifying inhibitors of neuronal degeneration useful for treating
PT e.g. Alzheimer's disease, by determining the ability of a compound to
PT induce nuclear factor kappa B activation, with the involvement of
PT presenilin or Par-4 -
XX
PS Claim 3; Page 61; 66pp; English.
XX
CC The invention relates to human Par-4 protein, presenilin protein (PS1
CC and PS2) and their corresponding DNA molecules. The invention also
CC relates to a method for identifying inhibitors of neuronal degeneration,
CC comprising cotransfecting eukaryotic host cells expressing presenilin
CC (PS), with a Par-4 DNA, and an NF-kappa B dependent reporter construct,
CC exposing the cotransfected cells to a candidate molecule and monitoring
CC the ability of the candidate molecule to induce NF-kappa B activation.
CC Presenilin proteins participates in nuclear factor kappa B (NF-kappa B)
CC signalling and activation. The inhibitors of neuronal degeneration
CC are useful for treating neurodegenerative disorders such as Alzheimer's
CC disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's
CC chorea, Down's syndrome, nerve deafness, Meniere's disease and also for
CC treating peripheral neuropathies, motorneuron disorders such as
CC amyotrophic lateral sclerosis (ALS), Bell's palsy and various conditions
CC involving spinal muscular atrophy and paralysis. The present DNA sequence
CC encodes human presenilin (PS2) protein.
XX
SQ Sequence 1346 BP; 263 A; 392 C; 388 G; 303 T; 0 other;

Query Match 14.9%; Score 224.2; DB 22; Length 1346;
Best Local Similarity 59.5%; Pred. No. 9.8e-42;

```
  Matches  398;  Conservative    0;  Mismatches  268;  Indels    3;  Gaps    1;

Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
              | | ||||||   |   || ||||||||||||    |||||  ||    || ||||||||  |
Db        224 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 283

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
              | | || ||||||    |||| ||    || || ||  |  |    || || |   | |
Db        284 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 343

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
              | ||||||   ||  |  | |       | ||      ||| |||  |    | |   ||
Db        344 AGAATGGA---CAGCTCATCTACACGACATTCACTGAGGACACACCCTCGGTGGGCCAGC 400

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
              |  |   ||  |    ||  | ||| ||||| |  ||||  ||||  | |||||
Db        401 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 460

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
              |  |  || | ||  |||| || |||   |  || ||| | || ||||| ||| | ||
Db        461 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 520

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
              |        |  | || || ||||| |||||    |||||  |    ||||| || || |
Db        521 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 580

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
                | | ||||| |       |      | ||| |     |  | ||||  || |
Db        581 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 640

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
              | || ||| |||| || || |||||  || ||  ||   |||||  |||  |||||| || |
Db        641 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 700

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
                ||   ||| || |||||  || ||  || ||||||||||| |||||  |||  | |  ||||
Db        701 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 760

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
              |  | |||   |  ||||| || |  ||||| || || |||||    || ||||| ||
Db        761 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 820

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
              |||||    |||| |||||||| ||||||||-|| ||||| || ||||| |
Db        821 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 880

Qy        791 ATTCGTCTG 799
              | || ||||
Db        881 ACTCATCTG 889


RESULT 37
AAD27447
ID   AAD27447 standard; cDNA; 1347 BP.
XX
AC   AAD27447;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human mutant presenilin 2 (PS2) cDNA #2.
XX
KW   Human; presenilin 2; PS2; amyloid precursor protein; APP; drug screening;
KW   Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
KW   Huntington's disease; amylotrophic lateral sclerosis; Picks disease;
KW   head injury disease; frontal lobe dementia; cerebellar degeneration;
KW   ischaemic injury; schizophrenia; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1347
FT                   /*tag=  a
FT                   /product= "Human mutant presenilin-2 protein"
FT                   /transl_except= (pos:1009..1101, aa:Xaa)
FT                   /transl_except= (pos:1102..1104, aa:Xaa)
FT                   /note= "Xaa corresponds to unknown amino acid"
XX
PN   WO200202601-A2.
XX
PD   10-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US16508.
XX
PR   30-JUN-2000; 2000US-215345P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Carter DB,  Tomasselli AG;
XX
DR   WPI; 2002-140082/18.
DR   P-PSDB; AAE17049.
XX
PT   Novel isolated mutant presenilin 1 and presenilin 2 polypeptides,
PT   useful for screening of drugs for treating pathologies associated with
PT   aberrant amyloid precursor protein processing, such as Alzheimer's
PT   disease  -
XX
PS   Claim 118; Page 72-73; 80pp; English.
XX
CC   The invention relates to mutant presenilin 1 (PS1) and presenilin 2
CC   (PS2) polypeptides. Presenilin are involved in the processing of amyloid
CC   precursor protein (APP) from which major amylodogenic peptides are
CC   cleaved. Mutant presenilins are useful for identifying agents that
CC   modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
CC   presenilin is also useful as a target for screening drugs useful in the
CC   treatment of pathologies associated with aberrant amyloid precursor
CC   protein processing, such as Alzheimer's disease, Parkinson's disease,
CC   multiple sclerosis, Huntington's disease, amylotrophic lateral sclerosis,
CC   head injury disease, Picks disease, frontal lobe dementia, cerebellar
CC   degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
CC   non-human animal is useful for analysing the interaction between APP and
CC   mutant presenilin-processing protease in vivo, and for screening anti-
CC   Alzheimer's disease drugs in vivo. A transgenic non-human
CC   animal is useful for analysing the interaction between APP and mutant
CC   presenilin-processing protease in vivo, and for screening anti-
CC   Alzheimer's disease drugs in vivo. The present sequence is human
CC   mutant PS2 cDNA.
XX
SQ   Sequence 1347 BP; 263 A; 390 C; 388 G; 300 T; 6 other;

  Query Match             14.9%;  Score 224.2;  DB 24;  Length 1347;
  Best Local Similarity   59.5%;  Pred. No. 9.8e-42;
  Matches  398;  Conservative    0;  Mismatches  268;  Indels    3;  Gaps    1;

Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
              | | ||||||   |   || ||||||||||||    |||||  ||    || ||||||||  |
Db        224 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 283

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
              | | || ||||||    |||| ||    || || ||  |  |    || || |   | |
Db        284 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 343

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
              | ||||||   ||  |  | |       | ||      ||| |||  |    | |   ||
Db        344 AGAATGGA---CAGCTCATCTACACGACATTCACTGAGGACACACCCTCGGTGGGCCAGC 400

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
              |  |   ||  |    ||  | ||| ||||| |  ||||  ||||  | |||||
Db        401 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 460

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
              |  |  || | ||  |||| || |||   |  || ||| | || ||||| ||| | ||
Db        461 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 520

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
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Db        521 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 580

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550

Db        581 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 640

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610

Db        641 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 700

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670

Db        701 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 760

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730

Db        761 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 820

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790

Db        821 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 880

Qy        791 ATTCGTCTG 799

Db        881 ACTCATCTG 889


RESULT 38
AAZ40670
ID   AAZ40670 standard; DNA; 1983 BP.
XX
AC   AAZ40670;
XX
DT   13-MAR-2000  (first entry)
XX
DE   Human presenilin-2 gene splice variant 2.
XX
KW   Central nervous system; CNS; presenilin-2 gene; screening; human;
KW   Alzheimer's disease; splice variant; ss.
XX
OS   Homo sapiens.
XX
PN   WO9960122-A1.
XX
PD   25-NOV-1999.
XX
PF   20-MAY-1999;   99WO-JP02627.
XX
PR   21-MAY-1998;   98JP-0139408.
XX
PA   (TANA ) TANABE SEIYAKU CO.
XX
PI   Takagi T,  Sato N,  Tohyama M;
XX
DR   WPI; 2000-072440/06.
XX
PT   Screening for remedies or preventives for central nervous system
PT   diseases, particularly Alzheimer's disease -
XX
PS   Claim 17; Page 34-35; 41pp; Japanese.
XX
CC   The invention provides a method for screening and identifying remedies or
CC   preventives for central nervous system (CNS) diseases. The method
CC   comprises assaying the inhibitory effect of a test substance on the
CC   expression of a splicing variety transcribed from presenilin-2 gene. The
CC   method is useful for screening remedies or preventives for CNS diseases,
CC   particularly Alzheimer's disease and for diagnosis of the disease. The
CC   present sequence represents a splice variant of human presenilin-2 gene.
XX
SQ   Sequence 1983 BP; 426 A; 523 C; 561 G; 473 T; 0 other;

  Query Match             14.9%;  Score 224.2;  DB 21;  Length 1983;
  Best Local Similarity   59.5%;  Pred. No. 1.1e-41;
  Matches  398;  Conservative    0;  Mismatches  268;  Indels    3;  Gaps    1;

Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190

Db        412 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 471

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250

Db        472 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 531

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310

Db        532 AGAATGGA---CAGCTCATCTACACGACATTCACTGAGGACACACCCTCGGTGGGCCAGC 588

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370

Db        589 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 648

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430

Db        649 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 708

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490

Db        709 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 768

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550

Db        769 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 828

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610

Db        829 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 888

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670

Db        889 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 948

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730

Db        949 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1008

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790

Db       1009 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1068

Qy        791 ATTCGTCTG 799

Db       1069 ACTCATCTG 1077


RESULT 39
AAZ40668
ID   AAZ40668 standard; DNA; 2144 BP.
XX
AC   AAZ40668;
XX
DT   13-MAR-2000  (first entry)
XX
DE   Human presenilin-2 gene sequence.
XX
KW   Central nervous system; CNS; presenilin-2 gene; screening; human;
KW   Alzheimer's disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9960122-A1.
XX
PD   25-NOV-1999.
XX
PF   20-MAY-1999;   99WO-JP02627.
XX
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PR   21-MAY-1998;   98JP-0139408.
XX
PA   (TANA ) TANABE SEIYAKU CO.
XX
PI   Takagi T,  Sato N,  Tohyama M;
XX
DR   WPI; 2000-072440/06.
XX
PT   Screening for remedies or preventives for central nervous system
PT   diseases, particularly Alzheimer's disease -
XX
PS   Disclosure; Fig 3; 41pp; Japanese.
XX
CC   The invention provides a method for screening and identifying remedies or
CC   preventives for central nervous system (CNS) diseases. The method
CC   comprises assaying the inhibitory effect of a test substance on the
CC   expression of a splicing variety transcribed from presenilin-2 gene. The
CC   method is useful for screening remedies or preventives for CNS diseases,
CC   particularly Alzheimer's disease and for diagnosis of the disease. The
CC   present sequence represents the human presenilin-2 gene sequence.
XX
SQ   Sequence 2144 BP; 461 A; 568 C; 618 G; 497 T; 0 other;

  Query Match           14.9%;  Score 224.2;  DB 21;  Length 2144;
  Best Local Similarity  59.5%;  Pred. No. 1.1e-41;
  Matches  398;  Conservative    0;  Mismatches  268;  Indels    3;  Gaps    1;

Qy       131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
Db       573 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 632

Qy       191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
Db       633 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 692

Qy       251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
Db       693 AGAATGGA---CAGCTCATCTACACGACATTCACTGAGGACACACCCTCGGTGGGCCAGC 749

Qy       311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
Db       750 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 809

Qy       371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
Db       810 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 869

Qy       431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
Db       870 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 929

Qy       491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
Db       930 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 989

Qy       551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
Db       990 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 1049

Qy       611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
Db       1050 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 1109

Qy       671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
Db       1110 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1169

Qy       731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
Db       1170 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1229

Qy       791 ATTCGTCTG 799
Db       1230 ACTCATCTG 1238


RESULT 40
AAT40031
ID   AAT40031 standard; DNA; 2229 BP.
XX
AC   AAT40031;
XX
DT   25-JUL-1997  (first entry)
XX
DE   Human presenilin-2 wild type coding sequence.
XX
KW   Presenilin-2; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;
KW   familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;
KW   depression; antibody; gene expression modulator; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             366..1712
FT                   /*tag= a
FT                   /product= presenilin-2
XX
PN   WO9634099-A2.
XX
PD   31-OCT-1996.
XX
PF   29-APR-1996;   96WO-CA00263.
XX
PR   31-JUL-1995;   95US-0509359.
PR   28-APR-1995;   95US-0431048.
PR   28-JUN-1995;   95US-0496841.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1996-497631/49.
DR   P-PSDB; AAW05762.
XX
PT   New presenilin genes - useful for diagnosis, therapy and drug
PT   screening of familial Alzheimer's disease, cerebral disorders, etc.
XX
PS   Claim 8; Page 148-150; 178pp; English.
XX
CC   This sequence represents the coding sequence for the human presenilin-2.
CC   AAT40028 and AAT40029 represent the coding sequences for the two
CC   different forms of wild type human presenilin-1 (PS-1). The form
CC   represented by AAT40029 results from alternate splicing of the genomic
CC   DNA sequence. AAT40030 represents the coding sequence for wild type mouse
CC   PS-1. The presenilins are a family of highly conserved integral membrane
CC   proteins with a common structural motif, common alternate splicing
CC   patterns, and common mutational hot spot regions. Mutations in PS genes
CC   are implicated in familial Alzheimer's disease (AD) and possibly other
CC   diseases such as cerebral haemorrhage, schizophrenia, depression etc., so
CC   detection of mutations in these sequences can be used for diagnosis of
CC   these diseases. The encoded proteins, or vectors that express them or
CC   containing antisense sequences, antibodies selective for mutant forms of
CC   the encoded proteins (such as AAW05736) and modulators of PS gene
CC   expression are potentially useful for treatment of AD etc. Transgenic
CC   animals are useful as models for drug screening. The antibodies can also
CC   be used e.g. for affinity purification and in immunoassays.
XX
SQ   Sequence 2229 BP; 481 A; 579 C; 633 G; 521 T; 15 other;

  Query Match           14.9%;  Score 224.2;  DB 17;  Length 2229;
  Best Local Similarity  59.5%;  Pred. No. 1.1e-41;
  Matches  398;  Conservative    0;  Mismatches  268;  Indels    3;  Gaps    1;

Qy       131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
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Db        589 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCATGTGATCATGCTGTTTGTGCCTG 648

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250

Db        649 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 708

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310

Db        709 AGAATGGA---CAGCTCATCTACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGC 765

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370

Db        766 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 825

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430

Db        826 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 885

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490

Db        886 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 945

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550

Db        946 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 1005

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610

Db       1006 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 1065

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670

Db       1066 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 1125

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730

Db       1126 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1185

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790

Db       1186 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1245

Qy        791 ATTCGTCTG 799

Db       1246 ACTCATCTG 1254


RESULT 41
AAV04669
ID   AAV04669 standard; cDNA; 2229 BP.
XX
AC   AAV04669;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human presenilin-2 cDNA (hPS2).
XX
KW   Presenilin-1; PS1 gene; human; familial Alzheimer's disease; FAD;
KW   cerebral haemorrhage; schizophrenia; depression; epilepsy;
KW   mental retardation; diagnosis; therapy; transgenic animal; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             366..1715
FT                   /*tag=  a
FT   mutation        787
FT                   /*tag=  p
FT                   /note= "A to T FAD mutation site (Asn141Ile)"
FT   mutation        1080
FT                   /*tag=  q
FT                   /note= "A to G FAD mutation site (Met239Val)"
FT   mutation        1624
FT                   /*tag=  r
FT                   /note= "T to C FAD mutation site (Ile420Thr)"
XX
PN   WO9801549-A2.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-CA00475.
XX
PR   02-JAN-1997;   97US-0034590.
PR   05-JUL-1996;   96US-0021673.
PR   12-JUL-1996;   96US-0021700.
PR   08-NOV-1996;   96US-0029895.
XX
PA   (HSCR-) HSC RES & DEV LP.
PA   (UTOR ) UNIV TORONTO GOVERNING COUNCIL.
XX
PI   Fraser PE,  Rommens JM,  St George-Hyslop PH;
XX
DR   WPI; 1998-286355/25.
DR   P-PSDB; AAW23967.
XX
PT   New isolated mutant presenilin-1 genes - useful for developing
PT   products for use in detection, diagnosis and therapy of Alzheimer's
PT   disease and for drug screening
XX
PS   Disclosure; Page 201-203; 238pp; English.
XX
CC   This cDNA clone, deposited as ATCC 97214, codes for human
CC   presenilin-2 (hPS2, see AAW23967).  Mutations in the presenilin genes
CC   have been linked to the development in humans of forms of familial
CC   Alzheimer's disease (FAD) and may be causative of other disorders,
CC   e.g. cognitive, intellectual, neurological or physiological
CC   disorders such as cerebral haemorrhage, schizophrenia, depression,
CC   mental retardation and epilepsy.  hPS2 cDNA has been obtained from
CC   CaCo2 cancer and human brain cDNA using primers based on ESTs
CC   identified using the human PS1 gene.  The PS2 gene maps to
CC   chromosome 1.  Human hPS1 sequences (see AAV04666-67) are also
CC   disclosed.  Use of the nucleic acids and proteins comprising or
CC   derived from the presenilins is made in screening and diagnosing
CC   FAD, identifying and developing therapeutics for treatment of FAD,
CC   and in producing cell lines and transgenic animals useful as models
CC   of FAD.  Nucleic acids (see AAV04674-80) encoding presenilin
CC   interacting proteins are also provided.
XX
SQ   Sequence 2229 BP; 481 A; 579 C; 632 G; 522 T; 15 other;

  Query Match           14.9%;  Score 224.2;  DB 19;  Length 2229;
  Best Local Similarity  59.5%;  Pred. No. 1.1e-41;
  Matches  398;  Conservative    0;  Mismatches  268;  Indels    3;  Gaps    1;

Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190

Db        589 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCATGTGATCATGCTGTTTGTGCCTG 648

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250

Db        649 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 708

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310

Db        709 AGAATGGA---CAGCTCATCTACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGC 765

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370

Db        766 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 825

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430

Db        826 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 885

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
```

```
Db        886 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 945

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550

Db        946 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 1005

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610

Db       1006 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 1065

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670

Db       1066 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 1125

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730

Db       1126 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1185

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790

Db       1186 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1245

Qy        791 ATTCGTCTG 799

Db       1246 ACTCATCTG 1254


RESULT 42
AAX75762
ID   AAX75762 standard; DNA; 2236 BP.
XX
AC   AAX75762;
XX
DT   22-JUL-1999  (first entry)
XX
DE   Human presenilin II DNA.
XX
KW   Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW   frameshift mutation; age-related disease; neurodegenerative disorder;
KW   Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW   Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW   diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW   ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW   neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW   glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW   bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW   high mobility group protein-C; neuroendocrine specific protein A; ss.
XX
OS   Homo sapiens.
XX
PN   WO9845322-A2.
XX
PD   15-OCT-1998.
XX
PF   02-APR-1998;   98WO-IB00705.
XX
PR   10-APR-1997;   97US-0043163.
XX
PA   (UYUT-) RIJKSUNIV UTRECHT.
PA   (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA   (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI   Burbach JPH,  Grosveld FG,  Van Leeuwen FW;
XX
DR   WPI; 1998-609901/51.
XX
PT   Diagnosing disease by detecting frameshift mutations in RNA or
PT   corresponding protein mutations - used to diagnose cancer and
PT   neurological diseases, particularly Alzheimer's disease, and also
PT   for treatment and prevention with specific ribozymes or wild-type
PT   RNA
XX
PS   Disclosure; Figure 11; 258pp; English.

XX
CC   This invention describes a novel method for the diagnosis of a disease
CC   caused by, or associated with, an RNA molecule that has a frameshift
CC   mutation. The method is used to diagnose age-related diseases,
CC   especially cancer and a wide range of neurodegenerative disorders (e.g.
CC   Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's
CC   disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus
CC   type II and many others listed) or susceptibility to these disorders. The
CC   method allows a definitive diagnosis of Alzheimer's disease in living
CC   patients, at an early stage. It is based on the observation that disease
CC   may be caused by mutations in RNA rather than DNA. The invention
CC   describes the used of neuronal system RNA molecules, specifically
CC   proteins including beta-amyloid precursor protein (beta-APP), the
CC   microtubule associated proteins Tau and Big Tau, ubiquitin B,
CC   apolipoprotein E, microtubule associated protein 2 (MAP2),
CC   neurofilament-L, neurofilament-M, neurofilament-F, presenilin I,
CC   presenilin II, glial fibrillary acidic protein (GFAP), the cellular
CC   tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene,
CC   semaphorin III, HUPF-1, high mobility group protein-C (HMGP-C) and
CC   neuroendocrine specific protein A. This sequence encodes the wild type
CC   and mutant protein fragments represented in AAY20896-Y20955.
XX
SQ   Sequence 2236 BP; 490 A; 583 C; 645 G; 518 T; 0 other;

  Query Match             14.9%;  Score 224.2;  DB 19;  Length 2236;
  Best Local Similarity   59.5%;  Pred. No. 1.1e-41;
  Matches  398;  Conservative    0;  Mismatches  268;  Indels    3;  Gaps    1;

Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190

Db        591 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 650

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250

Db        651 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 710

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310

Db        711 AGAATGGA---CAGCTCATCTACACGACATTCACTGAGGACACACCCTCGGTGGGCCAGC 767

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370

Db        768 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 827

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430

Db        828 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 887

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490

Db        888 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 947

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550

Db        948 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 1007

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610

Db       1008 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 1067

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670

Db       1068 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 1127

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730

Db       1128 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1187

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790

Db       1188 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1247

Qy        791 ATTCGTCTG 799
```

```
Db       1248 ACTCATCTG 1256

RESULT 43
AAD18121
ID   AAD18121 standard; DNA; 2236 BP.
XX
AC   AAD18121;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human presenilin-2 (PS-2) protein DNA.
XX
KW   Human; catenin p120; presenilin-2; PS-2; neuroprotective; gene therapy;
KW   neurodegenerative disease; Alzheimer's disease; nootropic; prophylaxis;
KW   neuronal disorder; cognitive disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             368..1714
FT                   /*tag= a
FT                   /product= "Human presenilin-2 protein"
XX
PN   WO200167097-A2.
XX
PD   13-SEP-2001.
XX
PF   09-MAR-2001; 2001WO-GB01059.
XX
PR   10-MAR-2000; 2000GB-0005895.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Hale RS,  Rowley A,  Blackstock W;
XX
DR   WPI; 2001-589954/66.
DR   P-PSDB; AAE10799.
XX
PT   Identifying presenilin or catenin p120 activity modulator useful for
PT   modulating presenilin-catenin p120 interaction and thus for treating
PT   cognitive disorder e.g., Alzheimer's disease comprises enhancing
PT   cognitive function -
XX
PS   Disclosure; Page 46-48; 48pp; English.
XX
CC   The invention relates to a method for identifying modulators of
CC   presenilin and catenin p120. Modulators of catenin p120 and presenilin
CC   are useful for the treatment and prophylaxis of disorders that is
CC   responsive to modulation of presenilin/catenin p120 activity. In
CC   particular, neuronal disorders such as cognitive disorders and
CC   neurodegenerative diseases such as Alzheimer's disease. Catenin p120 DNAs
CC   are useful for identifying mutations in catenin p120 genes.
CC   Identification of such mutations assist in the diagnosis of or
CC   susceptibility to Alzheimer's or other conditions associated with
CC   presenilin and in assessing the physiology of such disorders. Catenin
CC   p120 DNAs are also used in hybridisation studies to monitor expression of
CC   p120 genes and in particular for up or down regulation of catenin p120
CC   expression. The present DNA sequence encodes human presenilin-2 (PS-2)
CC   protein.
XX
SQ   Sequence 2236 BP; 490 A; 583 C; 645 G; 518 T; 0 other;

  Query Match             14.9%;  Score 224.2;  DB 22;  Length 2236;
  Best Local Similarity   59.5%;  Pred. No. 1.1e-41;
  Matches  398;  Conservative    0;  Mismatches  268;  Indels    3;  Gaps    1;

Qy       131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
Db       591 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 650

Qy       191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
Db       651 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 710

Qy       251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
Db       711 AGAATGGA---CAGCTCATCTACACGACATTCACTGAGGACACACCCTCGGTGGGCCAGC 767

Qy       311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
Db       768 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 827

Qy       371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
Db       828 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 887

Qy       431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
Db       888 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 947

Qy       491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
Db       948 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 1007

Qy       551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
Db       1008 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 1067

Qy       611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
Db       1068 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 1127

Qy       671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
Db       1128 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1187

Qy       731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
Db       1188 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1247

Qy       791 ATTCGTCTG 799
Db       1248 ACTCATCTG 1256


RESULT 44
AAH74994
ID   AAH74994 standard; DNA; 2236 BP.
XX
AC   AAH74994;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Nucleotide sequence of human presenilin 2.
XX
KW   KIAA0253; presenilin; Alzheimer's disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             368..1714
FT                   /*tag= a
FT                   /product= "presenilin 2"
XX
PN   WO200167109-A1.
XX
PD   13-SEP-2001.
XX
PF   09-MAR-2001; 2001WO-GB01057.
XX
PR   10-MAR-2000; 2000GB-0005894.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
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PI Hale RS, Rowley A, Blackstock W;
XX
DR WPI; 2001-522960/57.
DR P-PSDB; AAG63937.
XX
PT Identifying a modulator of presenilin function by determining the
PT ability of presenilin to bind to a K1AA0253 polypeptide in the presence
PT and absence of a test compound, useful in the treatment or prophylaxis
PT of Alzheimer's disease -
XX
PS Disclosure; Page 44-47; 48pp; English.
XX
CC The present sequence encodes human presenilin 2. KIAA0253 binds to
CC presenilin. The specification describes a method of identifying a
CC modulator of presenilin function or KIAA0253 function. The method
CC comprises determining presenilin activity or KIAA0253 activity
CC in the presence and absence of a test compound, where presenilin
CC activity is determined by its ability to bind to KIAA0253. A modulator
CC of presenilin or K1AA0253 polypeptide is useful in the manufacture of
CC a medicament for the treatment or prophylaxis of Alzheimer's disease.
CC The K1AA0253 polynucleotide and K1AA0253 polypeptide are useful in the
CC treatment, prophylaxis or diagnosis of Alzheimer's disease.
XX
SQ Sequence 2236 BP; 490 A; 583 C; 645 G; 518 T; 0 other;

Query Match 14.9%; Score 224.2; DB 22; Length 2236;
Best Local Similarity 59.5%; Pred. No. 1.1e-41;
Matches 398; Conservative 0; Mismatches 268; Indels 3; Gaps 1;

```
Qy       131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
Db       591 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 650

Qy       191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
Db       651 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 710

Qy       251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
Db       711 AGAATGGA---CAGCTCATCTACACGACATTCACTGAGGACACACCCTCGGTGGGCCAGC 767

Qy       311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
Db       768 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 827

Qy       371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
Db       828 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 887

Qy       431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
Db       888 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 947

Qy       491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
Db       948 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 1007

Qy       551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
Db       1008 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 1067

Qy       611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
Db       1068 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 1127

Qy       671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
Db       1128 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1187

Qy       731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
Db       1188 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1247
```

Qy 791 ATTCGTCTG 799
Db 1248 ACTCATCTG 1256

RESULT 45
AAH98480
ID AAH98480 standard; cDNA; 2527 BP.
XX
AC AAH98480;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 337.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR P-PSDB; AAM23821.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 429-430; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 2527 BP; 547 A; 650 C; 726 G; 604 T; 0 other;

Query Match 14.9%; Score 224.2; DB 22; Length 2527;
Best Local Similarity 59.5%; Pred. No. 1.2e-41;
Matches 398; Conservative 0; Mismatches 268; Indels 3; Gaps 1;

```
Qy       131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
Db       612 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCATGTGATCATGCTGTTTGTGCCTG 671

Qy       191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
Db       672 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 731

Qy       251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
Db       732 AGAATGGA---CAGCTCATCTACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGC 788
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Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
Db        789 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 848

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
Db        849 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 908

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
Db        909 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 968

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
Db        969 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 1028

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
Db       1029 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 1088

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
Db       1089 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 1148

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
Db       1149 TCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTC 1208

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
Db       1209 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 1268

Qy        791 ATTCGTCTG 799
Db       1269 ACTCATCTG 1277
```

RESULT 46
AAD27446
ID AAD27446 standard; cDNA; 1347 BP.
XX
AC AAD27446;
XX
DT 18-APR-2002 (first entry)
XX
DE Human mutant presenilin 2 (PS2) cDNA #1.
XX
KW Human; presenilin 2; PS2; amyloid precursor protein; APP; drug screening;
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
KW Huntington's disease; amylotrophic lateral sclerosis; Picks disease;
KW head injury disease; frontal lobe dementia; cerebellar degeneration;
KW ischaemic injury; schizophrenia; mutant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1347
FT /*tag= a
FT /product= "Human mutant presenilin-2 protein"
FT /transl_except= (pos:790..792, aa:Xaa)
FT /transl_except= (pos:793..795, aa:Xaa)
FT /note= "Xaa corresponds to unknown amino acid"
XX
PN WO200202601-A2.
XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US16508.
XX
PR 30-JUN-2000; 2000US-215345P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Carter DB, Tomasselli AG;
XX
DR WPI; 2002-140082/18.
DR P-PSDB; AAE17048.
XX
PT Novel isolated mutant presenilin 1 and presenilin 2 polypeptides,
PT useful for screening of drugs for treating pathologies associated with
PT aberrant amyloid precursor protein processing, such as Alzheimer's
PT disease -
XX
PS Claim 110; Page 72; 80pp; English.
XX
CC The invention relates to mutant presenilin 1 (PS1) and presenilin 2
CC (PS2) polypeptides. Presenilin are involved in the processing of amyloid
CC precursor protein (APP) from which major amylodogenic peptides are
CC cleaved. Mutant presenilins are useful for identifying agents that
CC modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
CC presenilin is also useful as a target for screening drugs useful in the
CC treatment of pathologies associated with aberrant amyloid precursor
CC protein processing, such as Alzheimer's disease, Parkinson's disease,
CC multiple sclerosis, Huntington's disease, amylotrophic lateral sclerosis,
CC head injury disease, Picks disease, frontal lobe dementia, cerebellar
CC degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
CC non-human animal is useful for analysing the interaction between APP and
CC mutant presenilin-processing protease in vivo, and for screening anti-
CC Alzheimer's disease drugs in vivo. A transgenic non-human
CC animal is useful for analysing the interaction between APP and mutant
CC presenilin-processing protease in vivo, and for screening anti-
CC Alzheimer's disease drugs in vivo. The present sequence is human
CC mutant PS2 cDNA.
XX
SQ Sequence 1347 BP; 264 A; 390 C; 386 G; 301 T; 6 other;

Query Match 14.8%; Score 221.4; DB 24; Length 1347;
Best Local Similarity 58.9%; Pred. No. 4.3e-41;
Matches 394; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

```
Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
Db        224 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 283

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
Db        284 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 343

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
Db        344 AGAATGGA---CAGCTCATCTACACGACATTCACTGAGGACACACCCTCGGTGGGCCAGC 400

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
Db        401 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 460

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
Db        461 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 520

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
Db        521 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 580

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
Db        581 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 640

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
Db        641 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 700

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
Db        701 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 760
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Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
              |  | |||   |  ||||| || |  |||      || |||||    || ||||| ||
Db        761 TCATCCTGGGCGCCATCTCTGTGTATGATNNNNNNGCTGTGCTGTGTCCCAAAGGGCCTC 820

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
              |||||   |||| |||||||| |||||||||| ||||| || ||||| || ||||| |
Db        821 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 880

Qy        791 ATTCGTCTG 799
              | || ||||
Db        881 ACTCATCTG 889


RESULT 47
AAD27448
ID   AAD27448 standard; cDNA; 1347 BP.
XX
AC   AAD27448;
XX
DT   18-APR-2002  (first entry)
XX
DE   Human mutant presenilin 2 (PS2) cDNA #3.
XX
KW   Human; presenilin 2; PS2; amyloid precursor protein; APP; drug screening;
KW   Alzheimer's disease; Parkinson's disease; multiple sclerosis; stroke;
KW   Huntington's disease; amylotrophic lateral sclerosis; Picks disease;
KW   head injury disease; frontal lobe dementia; cerebellar degeneration;
KW   ischaemic injury; schizophrenia; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1347
FT                   /*tag= a
FT                   /product= "Human mutant presenilin-2 protein"
FT                   /transl_except= (pos:790..792, aa:Xaa)
FT                   /transl_except= (pos:793..795, aa:Xaa)
FT                   /transl_except= (pos:1009..1101, aa:Xaa)
FT                   /transl_except= (pos:1102..1104, aa:Xaa)
FT                   /note= "Xaa corresponds to unknown amino acid"
XX
PN   WO200202601-A2.
XX
PD   10-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US16508.
XX
PR   30-JUN-2000; 2000US-215345P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Carter DB,  Tomasselli AG;
XX
DR   WPI; 2002-140082/18.
DR   P-PSDB; AAE17050.
XX
PT   Novel isolated mutant presenilin 1 and presenilin 2 polypeptides,
PT   useful for screening of drugs for treating pathologies associated with
PT   aberrant amyloid precursor protein processing, such as Alzheimer's
PT   disease -
XX
PS   Claim 126; Page 73; 80pp; English.
XX
CC   The invention relates to mutant presenilin 1 (PS1) and presenilin 2
CC   (PS2) polypeptides. Presenilin are involved in the processing of amyloid
CC   precursor protein (APP) from which major amylodogenic peptides are
CC   cleaved. Mutant presenilins are useful for identifying agents that
CC   modulate amyloid beta-peptide (Abeta) derived peptide production. Mutant
CC   presenilin is also useful as a target for screening drugs useful in the
CC   treatment of pathologies associated with aberrant amyloid precursor
CC   protein processing, such as Alzheimer's disease, Parkinson's disease,
CC   multiple sclerosis, Huntington's disease, amylotrophic lateral sclerosis,
CC   head injury disease, Picks disease, frontal lobe dementia, cerebellar
CC   degeneration, stroke, ischaemic injury and schizophrenia. A transgenic
CC   non-human animal is useful for analysing the interaction between APP and
CC   mutant presenilin-processing protease in vivo, and for screening anti-
CC   Alzheimer's disease drugs in vivo. A transgenic non-human
CC   animal is useful for analysing the interaction between APP and mutant
CC   presenilin-processing protease in vivo, and for screening anti-
CC   Alzheimer's disease drugs in vivo. The present sequence is human
CC   mutant PS2 cDNA.
XX
SQ   Sequence 1347 BP; 263 A; 388 C; 386 G; 298 T; 12 other;

  Query Match           14.8%;  Score 221.4;  DB 24;  Length 1347;
  Best Local Similarity   58.9%;  Pred. No. 4.3e-41;
  Matches  394;  Conservative    0;  Mismatches  272;  Indels    3;  Gaps    1;

Qy        131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
              | | ||||||  .|   || ||||||||||||    ||||| ||    || ||||||||
Db        224 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTTTGTGCCTG 283

Qy        191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
              |  | || ||||||    |||| ||    || || ||  |  |    || || |   | |
Db        284 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 343

Qy        251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
              | ||||||   ||  |  | |       | ||       ||| |||  |    | |   ||
Db        344 AGAATGGA---CAGCTCATCTACACGACATTCACTGAGGACACACCCTCGGTGGGCCAGC 400

Qy        311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
                  | |  ||  |    ||  | ||| ||||| |  ||||  ||||  | |||||
Db        401 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 460

Qy        371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
              |  |  || | ||  |||| || |||   |  || ||| | || ||||| ||| | ||
Db        461 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCA 520

Qy        431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
              |         |  | || || ||||| |||||    |||||  |    |||||| || || |
Db        521 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 580

Qy        491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
              | | ||||| |      |  |      | ||| |      |  | |||| || |
Db        581 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 640

Qy        551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
              | || ||| |||| || || ||||| || ||  ||   ||||| |||  |||||| || |
Db        641 TGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCA 700

Qy        611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
              ||   ||| || ||||| || || || ||||||||||| ||||| ||| | | ||||
Db        701 TGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGG 760

Qy        671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
              |  | |||   |  ||||| || |  |||      || |||||    || ||||| ||
Db        761 TCATCCTGGGCGCCATCTCTGTGTATGATNNNNNNGCTGTGCTGTGTCCCAAAGGGCCTC 820

Qy        731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
              |||||   |||| |||||||| |||||||||| ||||| || ||||| || ||||| |
Db        821 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATAT 880

Qy        791 ATTCGTCTG 799
              | || ||||
Db        881 ACTCATCTG 889


RESULT 48
AAT87401
ID   AAT87401 standard; DNA; 1417 BP.
XX
AC   AAT87401;
XX
DT   07-DEC-1997  (first entry)
```

```
XX
DE   AD4/AD3LP sequence.
XX
KW   AD3; AD4/AD3LP; Alzheimer's disease; chromosome; missegregation;
KW   presenilin; inhibitor; AD; trisomy 21; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1132
FT                   /*tag=  a
XX
PN   WO9707213-A2.
XX
PD   27-FEB-1997.
XX
PF   15-AUG-1996;   96WO-US13314.
XX
PR   16-AUG-1995;   95US-0002448.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Li J,  Potter H;
XX
DR   WPI; 1997-165297/15.
DR   P-PSDB; AAW28506.
XX
PT   Identifying genes which cause chromosome missegregation - useful for
PT   identifying causes of and treatments for diseases, e.g. Alzheimer's
PT   disease, cancer and ageing
XX
PS   Claim 16; Fig 1; 77pp; English.
XX
CC   Identifying genes which cause improper chromosome segregation,
CC   screening for inhibitors of chromosome missegregation and processes
CC   caused by genes encoding chromosome missegregation promoters
CC   was exemplified using Alzheimer's disease.  The sequences
CC   given in AAT87401 to AAT87426 can be used in the above methods.
CC   It is not clear from the figure legend, the figure and the
CC   disclosure of the specification which sequence of Fig 1 and Fig 28
CC   is the AD4/AD3LP or the AD3 sequence.
XX
SQ   Sequence 1417 BP; 307 A; 385 C; 380 G; 345 T; 0 other;

  Query Match           12.9%;  Score 192.8;  DB 18;  Length 1417;
  Best Local Similarity  56.6%;  Pred. No. 1.6e-34;
  Matches  378;  Conservative    0;  Mismatches  287;  Indels    3;  Gaps    1;

Qy       131 TTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCACGTTATTCATCTATTTGTGCCGG 190
Db        27 TGGAGGAAGAGCTGACCCTCAAATACGGAGCGAAGCACGTGATCATGCTGTGTGTGCCTG 86

Qy       191 TGTCACTATGCATGGCTCTGGTTGTTTTTACGATGAACACGATTACGTTTTATAGTCAAA 250
Db        87 TCACTCTGTGCATGATCGTGGTGGTAGCCACCATCAAGTCTGTGCGCTTCTACACAGAGA 146

Qy       251 ACAATGGAAGGCATTTACTATCACATCCTTTTGTCCGGGAAACAGACAGTATCGTTGAGA 310
Db       147 AGAATGGA---CAGCTCATCTACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGC 203

Qy       311 AGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAG 370
Db       204 GCCTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCA 263

Qy       371 TTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTG 430
Db       264 TCTTCTTGGTGGTGCTCTACAAGTACCGCTGCTACAAGTTCATCCATGGGTGGTTGATCA 323

Qy       431 TCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAA 490
Db       324 TGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGA 383

Qy       491 GTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTC 550
Db       384 CCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAG 443

Qy       551 TCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTA 610
Db       444 TGGGGCATGGTGTGATCCACTGGAAGGGCCCTCTGGTGCTGGAGCAGGCCTACCTCATCA 503

Qy       611 CAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGT 670
Db       504 TGATCAGTGCGCTCATGCCCCTAATGTTCATCAAGTACCCTCCAGAGTGGTCCGCGTGGG 563

Qy       671 TTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCAT 730
Db       564 TGATCCTGGCGCCCATCTCTGTGTATGATCTCGTGACTGTCCTGTGTTCCACAGGGCCTC 623

Qy       731 TGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTT 790
Db       624 TGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGACCATATTCTCTCCCCTGATAT 683

Qy       791 ATTCGTCT 798
Db       684 ACTCATCT 691


RESULT 49
AAZ40671
ID   AAZ40671 standard; DNA; 1848 BP.
XX
AC   AAZ40671;
XX
DT   13-MAR-2000  (first entry)
XX
DE   Human presenilin-2 gene splice variant 3.
XX
KW   Central nervous system; CNS; presenilin-2 gene; screening; human;
KW   Alzheimer's disease; splice variant; ss.
XX
OS   Homo sapiens.
XX
PN   WO9960122-A1.
XX
PD   25-NOV-1999.
XX
PF   20-MAY-1999;   99WO-JP02627.
XX
PR   21-MAY-1998;   98JP-0139408.
XX
PA   (TANA ) TANABE SEIYAKU CO.
XX
PI   Takagi T,  Satō N,  Tohyama M;
XX
DR   WPI; 2000-072440/06.
XX
PT   Screening for remedies or preventives for central nervous system
PT   diseases, particularly Alzheimer's disease -
XX
PS   Claim 18; Page 36-37; 41pp; Japanese.
XX
CC   The invention provides a method for screening and identifying remedies or
CC   preventives for central nervous system (CNS) diseases. The method
CC   comprises assaying the inhibitory effect of a test substance on the
CC   expression of a splicing variety transcribed from presenilin-2 gene. The
CC   method is useful for screening remedies or preventives for CNS diseases,
CC   particularly Alzheimer's disease and for diagnosis of the disease. The
CC   present sequence represents a splice variant of human presenilin-2 gene.
XX
SQ   Sequence 1848 BP; 393 A; 497 C; 513 G; 445 T; 0 other;

  Query Match           12.8%;  Score 192.2;  DB 21;  Length 1848;
  Best Local Similarity  63.1%;  Pred. No. 2.4e-34;
  Matches  296;  Conservative    0;  Mismatches  173;  Indels    0;  Gaps    0;

Qy       331 AATGCTCTCGTCATGTTGTGCGTGGTCGTTCTGATGACAGTTCTGCTGATTGTTTTCTAT 390
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Db        474 AACACCCTCATCATGATCAGCGTCATCGTGGTTATGACCATCTTCTTGGTGGTGCTCTAC 533

Qy        391 AAATACAAGTTTTATAAGCTTATTCATGGATGGCTTATTGTCAGCAGTTTTCTTCTTCTT 450

Db        534 AAGTACCGCTGCTACAAGTTCATCCATGGCTGGTTGATCATGTCTTCACTGATGCTGCTG 593

Qy        451 TTCCTATTCACTACAATCTATGTGCAAGAAGTTCTGAAAAGTTTCGATGTGTCTCCCAGC 510

Db        594 TTCCTCTTCACCTATATCTACCTTGGGGAAGTGCTCAAGACCTACAATGTGGCCATGGAC 653

Qy        511 GCACTATTGGTTTTGTTTGGACTGGGTAACTATGGAGTTCTCGGAATGATGTGTATACAT 570

Db        654 TACCCCACCCTCTTGCTGACTGTCTGGAACTTCGGGGCAGTGGGCATGGTGTGCATCCAC 713

Qy        571 TGGAAAGGTCCATTGCGTCTGCAACAGTTCTACCTTATTACAATGTCTGCACTAATGGCT 630

Db        714 TGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCATCATGATCAGTGCGCTCATGGCC 773

Qy        631 CTGGTCTTTATCAAGTACCTACCAGAATGGACTGTGTGGTTTGTGCTGTTTGTTATCTCG 690

Db        774 CTAGTGTTCATCAAGTACCTCCCAGAGTGGTCCGCGTGGGTCATCCTGGGCGCCATCTCT 833

Qy        691 GTTTGGGATCTGGTTGCCGTGCTCACACCAAAAGGACCATTGAGATATTTGGTGGAAACT 750

Db        834 GTGTATGATCTCGTGGCTGTGCTGTGTCCCAAAGGGCCTCTGAGAATGCTGGTAGAAACT 893

Qy        751 GCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTGATTTATTCGTCTG 799

Db        894 GCCCAGGAGAGAAATGAGCCCATATTCCCTGCCCTGATATACTCATCTG 942
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RESULT 50
AAZ40669
ID   AAZ40669 standard; DNA; 2002 BP.
XX
AC   AAZ40669;
XX
DT   13-MAR-2000  (first entry)
XX
DE   Human presenilin-2 gene splice variant 1.
XX
KW   Central nervous system; CNS; presenilin-2 gene; screening; human;
KW   Alzheimer's disease; splice variant; ss.
XX
OS   Homo sapiens.
XX
PN   WO9960122-A1.
XX
PD   25-NOV-1999.
XX
PF   20-MAY-1999;   99WO-JP02627.
XX
PR   21-MAY-1998;   98JP-0139408.
XX
PA   (TANA ) TANABE SEIYAKU CO.
XX
PI   Takagi T,  Sato N,  Tohyama M;
XX
DR   WPI; 2000-072440/06.
XX
PT   Screening for remedies or preventives for central nervous system
PT   diseases, particularly Alzheimer's disease -
XX
PS   Claim 16; Page 33-34; 41pp; Japanese.
XX
CC   The invention provides a method for screening and identifying remedies or
CC   preventives for central nervous system (CNS) diseases. The method
CC   comprises assaying the inhibitory effect of a test substance on the
CC   expression of a splicing variety transcribed from presenilin-2 gene. The
CC   method is useful for screening remedies or preventives for CNS diseases,
CC   particularly Alzheimer's disease and for diagnosis of the disease. The
CC   present sequence represents a splice variant of human presenilin-2 gene.
XX
SQ   Sequence 2002 BP; 430 A; 521 C; 588 G; 463 T; 0 other;
```

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  Query Match           10.9%;  Score 162.8;  DB 21;  Length 2002;
  Best Local Similarity   63.6%;  Pred. No. 1.3e-27;
  Matches  248;  Conservative    0;  Mismatches  142;  Indels    0;  Gaps    0;

Qy        410 TTATTCATGGATGGCTTATTGTCAGCAGTTTTCTTCTTCTTTTCCTATTCACTACAATCT 469

Db        707 TCATCCATGGCTGGTTGATCATGTCTTCACTGATGCTGCTGTTCCTCTTCACCTATATCT 766

Qy        470 ATGTGCAAGAAGTTCTGAAAAGTTTCGATGTGTCTCCCAGCGCACTATTGGTTTTGTTTG 529

Db        767 ACCTTGGGGAAGTGCTCAAGACCTACAATGTGGCCATGGACTACCCCACCCTCTTGCTGA 826

Qy        530 GACTGGGTAACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTC 589

Db        827 CTGTCTGGAACTTCGGGGCAGTGGGCATGGTGTGCATCCACTGGAAGGGCCCTCTGGTGC 886

Qy        590 TGCAACAGTTCTACCTTATTACAATGTCTGCACTAATGGCTCTGGTCTTTATCAAGTACC 649

Db        887 TGCAGCAGGCCTACCTCATCATGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACC 946

Qy        650 TACCAGAATGGACTGTGTGGTTTGTGCTGTTTGTTATCTCGGTTTGGGATCTGGTTGCCG 709

Db        947 TCCCAGAGTGGTCCGCGTGGGTCATCCTGGGCGCCATCTCTGTGTATGATCTCGTGGCTG 1006

Qy        710 TGCTCACACCAAAAGGACCATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAGC 769

Db       1007 TGCTGTGTCCCAAAGGGCCTCTGAGAATGCTGGTAGAAACTGCCCAGGAGAGAAATGAGC 1066

Qy        770 CAATTTTCCCGGCGCTGATTTATTCGTCTG 799

Db       1067 CCATATTCCCTGCCCTGATATACTCATCTG 1096
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Job time : 378 secs
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